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Query Match
Best Local Similarity 100.
Matches 1137; Conservative
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                                                                                           June 7, 2004, 17:16:51; Search time 38.8905 Seconds (without alignments) 8225.189 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_PMEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_PMEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9F_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-902-481A-5
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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             APPLICANT: Shimaoka, Motomu APPLICANT: Shimaoka, Motomu APPLICANT: Shifman, Julia APPLICANT: Shifman, Julia APPLICANT: Shifman, Julia APPLICANT: Mayo, Stephen Brown Stark Mayo, Stephen Brown Brown Mayora, PROFEINS WITH INTEGRIN-LIKE ACTIVITY FILE REFERENCE: A-70586-1/RFT/RMS/RMK CURRENT PILING DATE: 2001-07-09 PRIOR APPLICATION NUMBER: US 60/216,600 PRIOR PILING DATE: 2000-07-07 NUMBER OF SEQ ID NOS: 7

SOFTWARR: Patentin version: 3.1

SEQ ID NO 4
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ORGANISM: Artificial sequence
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    Springer, Timothy
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Best Local Similarity 99.5
Matches 1131; Conservative
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> Sequence 4, Application US/09902481A Publication No. US20030054440A1 GENERAL INFORMATION: RESULT 2 US-09-902-481A-4

### 1992-09 2004 ##################################	Page	East,	181 RIHFTEKZPONNDNPRSLIKPITOLLGRTHTATGLRKYVRELFNITNGARKNAFKILFLL 240 197 RIHFTEKRONDNPRSLIKPITOLLGRTHTATGLRKYVRELFNITNGARKNAFKILVIT 256	41 TDGEKFGDPLGYBDVI PELDREGVIRYVLGFGDAFRSEKSROBLATVASKPPRDHVFQAN 30	TOGEKGGPELOYEDVEPRADREGVIRYVLGVGDAFRSEKSKURLINIASKFFRDHVFQVN NPRALKTYONDLREKIFALEGTOTGSSSFRHEMSORGPESAALTSNGFLLSTVGSYDWAG	317 NFEALKTIONOLREKIFAIBGTOTGSSSSFEHEMSGEGFSAAITSNGFLLSTVGSYDWAG 376 361 GVPLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVOSLVLGAPRYOHIGLVAMFR 420 311 NFEALSTPINMTRVDSDMNDAYLGYAAAIILRNRVOSLVLGAPRYOHIGLVAMFR 436 311 NFEALSTPINMTRVNGSDMNDAYLGYAAAIILDNRVOSLVIKABPRYOHIGIVAMRR 436	21 ONTGWESNANVKGTOLGAFGASLGSVDVSNGSTDLVLIGAPHYYEOTRGGGVSVCPL 48	PRGGRARWQCDAVLYGGOOPWGRFGAALTVLGDVNGDKLTDVAIGAI 	ш	601 PVLRVKAIMBENDREVARNVFBCNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 660 	661 YDLALDSGRPHSRAVFNETKNSTRROTOVLGLTOTCETLKLOLPNCIBDPVSPIVLRLNF 720 	721 SLVGTPLSARGNLRPVLAEDAQRLPTALPPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780 	781 GPREFNVTVTVRNDGEDSYRTQVTFFFLDLSYRKYSTLQNQRSQRSWRLACESASSTEV 840 	941 SGALKSTSCSINHPIPPENSEVTENITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF 900	901 QLELPVKYAVYMVYTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGGRELPISLVFLVPV 960 	961 RINGTVIMDRPQVIPSENLSSTCHTKERLPSHSDPLABLRKAPVVNCSIAVCQRIQCDIP 1020	1021 FPGIORBENATLKGKLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGOGAFVRSQTET 1080 	1081 KVBPFBVPNPLPLIVGSSVGGLILLALITAALYKLGPFKROYKDMMSBGGPPGABPQ 1137 	RESULT 4 US-09-902-481A-1 Forgrance 1. Application US/09902481A Fublication No. US2030054440A1 GENERAL INFORMATION:	JCANT: Springer, Timothy JCANT: Shimaoka, Motomu JCANT: Shifman, Julia
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Morica
TITLE OF INVENTION: NO. US20030077278Alel Human 2
FILE REPRENCE: 27866/35004
CURRENT APPLICATION NUMBER: U$/09/891,943
CURRENT FILING DATE: 1998:11-16
PRIOR PRIOR APPLICATION NUMBER: 08/286,889
PRIOR PLING DATE: 1998:11-16
PRIOR PRILING DATE: 1994-10-05
PRIOR PRILING DATE: 1994-12-21
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Best Local Similarity 98.9%; Pred. No. 0;
Matches 1124; Conservative 8; Mismatches
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US-09-891-943-3
Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 1153
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Best Local Similarity 98.9
Matches 1124; Conservative
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                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat peptide;
; LOCATION: (1.7)..()
; OTHER INFORMATION:
US-09-902-481A-1
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; PRIOR APPLICATION WUMBER: US 09/758,493
; PRIOR PILING DATE: 2001-01-11
; PRIOR PILING DATE: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PSECSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1153
; TYPE: PRI
CREANISM: Homo sapiens
US-10-144-259-30
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Publication No. US20030109691A1
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REPERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
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APPLICANT: Spiringer, Timothy
APPLICANT: Shimaoka, Motcomu
APPLICANT: Shimaoka, Motcomu
APPLICANT: Shimaoka, Motcomu
APPLICANT: Shimaoka, Motcomu
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-10586-1/RFF/RMS/RWK
CURRENT APPLICATION NUMBER: US 60/9/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 5
LENGTH: 1137
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ORGANISM: Artificial
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                  RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAPKILFLL
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SGALKSTSCSINHPIPPENSEVTPNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 176, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS FILE REFERENCE: 390069,401C.
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
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Pred. No. 0;
B; Mismatches
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SEQ ID NO 176
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Best Local Similarity 98.9'
Matches 1124; Conservative
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CRGANISM: Homo sapiens
US-10-207-655-176
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US-10-207-655-176
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US-09-902-481A-6
| Sequence 6, Application US/09902481A
| Sequence 6, Application US/09902481A
| Publication No. US20030054440A1
| GENERAL INFORMATION:
| APPLICANT: Sprimacka, Motomu
| APPLICANT: Shifman, Julia
| APPLICANT: Mayo, Stephen
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| FILE REFERENCE: A-70586-1/RFT/RMS/RMK
| CURRENT FILING DATE: 2001-07-07
| PRIOR FILING DATE: 2001-07-07
| SUPPRINCE PARENTIN NUMBER: US 60/216,600
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 6
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99.2%; Score 5832; D
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1122; Conservative 9; Mismatches
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ORGANISM: Artificial sequence
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US-09-902-481A-6
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                                                        FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                 Gaps
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    Length 1137;
                              Indels
                              9
    DB 10;
 Score 5836; DB Pred. No. 0; 7; Mismatches
 99.38;
                            Matches 1124; Conservative
 Query Match
Best Local Similarity
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                                                                                                                                           197 RIHFTFKEFQNNPNDRSLVKDITGLIGRATHTATGIRKVVRELFNITNGARKNAFKILVVI
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Fatent No. USCO020123614A1

GENERAL INFORMATION:

APPLICANT: Springer, Timothy A.

APPLICANT: Simmaoka, Motcomu

APPLICANT: Simmaoka, Motcomu

APPLICANT: Lu, Chafen

TITLE OF INVENTION: DESIRED POLYPEPTIDES STABILIZED IN A

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME

FILE REFERENCE: CBN-002CP

CURRENT APPLICATION NUMBER: US/09/945,265

CURRENT PILING DATE: 2001-08-31

FRIOR FILING DATE: 2000-09-01

FRIOR FILING DATE: 2000-09-01

SEQ ID NO 4

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SEQ ID NO 4

SEQ ID NO 4
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                                                                     PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
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Pred. No. 0;
8; Mismatches
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Elarity 98.8%;
Conservative 8
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1123; Conserv
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US-09-945-265-4
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                                                                           TLVGKPLIAFRNIRPMLAALAQRYFTASLPFEKNCGADHICQDNLGISFSFPGLKSLLVG
677 LDLALDPGRISPRATFORTKNRSLSRVRVLGLKAHCENFNLLLPSCVEDSVTPITLRLNF
                                                 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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Patent No. US20020062008A1
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
PILE OF INVENTION: No. US20020062008A1el Human 2
TITLE OF INVENTION: No. US20020062008A1el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 08/193,043
ERALIER FILING DATE: 1994-00-05
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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               Sequence 204, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Elan Pharmaceutical Technology

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

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TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: 2002-10-04

NUMBER OF SED IN VOS: 349

SOFTWARE PatentIn version 3.1

SEQ ID NO 204

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CRGANISM: Homo sapiens
US-10-116-275-204
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                                       GAPLYPPNWSPTPINWSQENVDWRDSYLGYSTELALWKGVQSLVLGAPRYQHIGKAVIFI
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RESULT 13
US-09-891-943-4
Sequence 4, Application US/09891943
Publication No. US20030077278A1
GENERAL INFORMATION:

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420 120 197 300 377 437 480 497 540 556 900 616 676 9 79 80 GLOVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGFT--QLTQR TDGKKEGDSLDYKDVI PMADAAGI IRYAI GVGLAFQNRNSWKELND IASKPSQEHI FKVE RLOVPVEAVNINGLGISLAATTSPPOLLACGPTVHOTCSENTYVKGLCFLFGSNLRQQPQK RIHPTEKEFONNPNPRSLIKPITOLLGRIHTATGLRKVVRBLFNITNGARKNAFKILFLL TDGBKFGDPLGYEDVI PELDREGVI RYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMPR HCTSGSGISPSHSQRIAGSKLSPRLQYPGQSLSGGQDLTMCGLVDLTVGAQGHVLLLRSQ PVLRVKAIMBFNPRBVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT FNLDTENAMTFOENARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSBBF NFBALKTVQNQLREKIFA1EGTQTGSSSSFEHEMSQEGFSAA1TSNGPLLSTVGSYDWAG ONTGMMESNANVKGTOIGAYPGASLCSVDVDSNGSTDLV1.1GAPHYYEQTRGGQVSVCPL PRGQRARWQCDAVLYGEQGQPWGRPGAALTVLGDVNGDXLTDVAIGAPGEEDNRGAVYLP 661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF Gaps . 9 Length 1163; Indels tch 58.2%; Score 3423; DB 10; al Similarity 60.2%; Pred. No. 2.8e-307; 680; Conservative 149; Mismatches 294; Human APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278Alel Hum
PILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 2001-06-26
PRIOR PELLING DATE: 1998-11-16
PRIOR PILING DATE: 1994-11-16
PRIOR PLING DATE: 1994-08-05
PRIOR PLING DATE: 1994-12-21
PRIOR PLING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET. 2.0) ORGANISM: Homo sapiens US-09-891-943-4 20 61 198 301 318 438 557 181 241 258 361 421 481 541 601 617 TYPE: PRT Query Match Local Best Loca Matches 8 윰 ð 셤

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TCSLSYVAGAPQYKHHG--AVFELQKEGREASFLPVLEGEQMGSYFGSELCPVDIDMDGS 528
                                                                                                                                                                                                                                                                                                       subunit.";
. Biol. Chem. 268.2989-2996(1993).
. Biol. Chem. 268.2989-1994-1/BETA-1 IS A RECEPTOR FOR LAWININ AND
.- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAWININ AND
.- COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-P-P-G-
                                                              SQDKLTDVAIGAPLEGFGADDGASFGSVYIYNG-HWDGLSASFSQRIRASTVAPGLQYFG
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                                                                                                                     NGDKLTDVAIGAP----GEEDNR--GAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFG
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MEDLINE=33155124; PubMed=8428973;
Briesewitz R., Epstein M.R., Marcantonio E.E.;
Expression of native and truncated forms of the human integrin alpha 1 subunit.";
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a)
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Catarrhini; Hominidae;
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Mammalia; Butheria; Primates;
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DOMAIN. INTEGRINS
HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
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1 1113 EXTRACELLULAR (POTENTIAL).
                                              -: SUBCELLULAR LOCATION: Type I membrane protein.
-: DOMAIN: THE INTEGRIN I DOMAIN (INSERT) IS A VWFA DOMAIN WITH I - DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-: SIMILARITY: Belongs to the integrin alpha chain family.
-: SIMILARITY: Contains 1 VWFA domain.
-: SIMILARITY: Contains 7 FG-GAP repeats.
-: AIMILARITY: Contains 7 FG-GAP repeats.
-: DATABASE: NAME-PROW; NOTB-CD gaide CD49a entry;
WWWH-"http://www.ncbi.nlm.nih.gov/prow/cd/cd49a.htm".
                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0008305; C: integrin complex; TAS.
GO; GO: 0008305; F: cell adhesion receptor activity; NAS.
GO; GO: 0005518; F: cell adhesion receptor activity; NAS.
GO; GO: 0007160; P: cell-matrix adhesion; NAS.
InterPro; IPR002015; UWF A.
InterPro; IPR002015; UWF A.
Fram; PP00319; F: G-GAP; 3.
Fram; PP00319; F: cell-matrix alpha.
Fram; PF00319; F: cell-matrix alpha; F: SMRT; SM00191; Int. alpha; F: SMRT; SM00191; Int. alpha; F: SMRT; SM00121; INTEGRIN ALPHA; I.
PROSITE; PS00242; INTEGRIN ALPHA; I.
PROSITE; PS00242; UWFA; I.
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                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R GO; GO:0004895; E:cll adhesion receptor activity; TAS.
R GO; GO:0004895; F:cell adhesion receptor activity; TAS.
R InterPro; IPR00413; Integrin alpha.
R InterPro; IPR00413; Integrin alpha.
R Pfam; PF0189; FG-GAP; 3.
R Pfam; PF00357; NITEGRINA.
R PRINTS; PR00453; VWFADONAIN.
R PRINTS; PR00453; VWFADONAIN.
R SMART; SM00191; Int. alpha; 3.
SMART; SM00191; Int. alpha; 3.
SMART; SM00191; Int. alpha; 3.
R PROSITE; PS00242; INTEGRINA ALPHA; 1.
R PROSITE; PS00244; VWFA; 1.
R PROSITE; PS00245; VWFA; 1.
R PROSITE; PS004045; VWFA; 1.
R PROSIT
 novel gene within the common cystinosis-causing deletion. ^{\rm H}_{\rm J} Genome Res. 10:165-173 (2000).
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INTEGRIN ALPHA-E LIGHT CHAIN.
INTEGRIN ALPHA-E HEAVY CHAIN.
EXTRACELLULAR (FOTENTIAL).
POTENTIAL.
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GLU-RICH (ACIDIC).
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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                                                       MUTAGENESIS OF ASP-109 AND PHE-316.
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EMBL, AF168797; AAF43107.1; -.
PIR, A53213; A53213.
HSSP, P11215; 1A8X.
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19.5%; Score 1163; DB 1; Length 1179;
Best Local Similarity 28.8%; Pred. No. 2.7e-69;
Matches 356; Conservative 221; Mismatches 481; Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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larity 29.1%; Pred. No. 1.8e-69;
Conservative 213; Mismatches 465; Indels 205;
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LSST-----CHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQESFNATLK 1049
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                                                                                                                                                                                                                                                                                                        YMTNYALNYPRNLQPKKI-----QXPVSPDVQCDDPKPV---ASVLVMNCKIGHPIL-K 906
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                                                                                                                  GGSFLCEHFWLISTEEL----CEEDCFSNITIKVIYE-----PQTSGGRRDYPNFT--D
                                         -----TKORORLQCEDSSGCQSCLRKWN
                                                                                                                                                                          757 AQRLFTALF - PFEKNCGNDNICQDDLSITFSFMSLDCLYVGGPREFNVTVTVRNDGSDS
                                                                                   -------BILKIQLPNCIBDPVSPIVLRLNFSLVGTPLSAFGNLR----PVLAED
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MEDLINE-2013496; PubMed=10673275;
MININE-2013496; PubMed=10673275;
MININE-2013496; Anikater Y., Dietrich N.L., Maduro V.V., McDowell G., Shotelersuk V., Bouffard G.G., Beckstrom-Sternberg S.M., Gahl W.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shaw S.K., Cepek K.L., Murphy B.A., Russell G.J., Brenner M.B.,
Parker C.M.;
Wholecular cloning of the human mucosal lymphocyte integrin alpha
subunit. Unusual structure and restricted RNA distribution.";
J. Biol. Chem. 269:6016-6025(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen} (HML-1
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TISSUEL-Leukemia, and Lymphocytes;
WEDLINE-94164962; PubMed-8119947;
Shaw S.K., Cepek K.L., Murphy B.A., Russell G.J., Brenner M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fairer C.M.;
Submitted (MAR-1999) to the BMBL/GenBank/DDBJ databases
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1039 GIQBEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTBTKV 1098
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                                                                                                                                                           INWFGRSIHGWRDLGGDRLADVVVGABGRVVVLSSRPVVDVVTELSFSPEEIPVHEVECS 635
LCSVDVDSNGSTDLVLIGAPHYYBOTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGR 520
                                                                                                                                            FGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPR 580
                                                                                                                                                                                                581 LOYPGOSLSGGODLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECN 640
                                                                                                                                                                                                                                                   641 DQVVKGKEAG-EVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNST 699
                                                                                                                                                                                                                                                                     636 YSAREEQKHGVKLKACFRIKPLIPQ--PQGRLLANLSYTLQLDGHRMRSRGLFPDGSHEL 693
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28.FBB-2003 (Rel. 41, Last annotation update)
Integrin alpha-E precursor (Integrin alpha M290).
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SEQUENCE FROM N.A. STRAIN=AKR; MBDLINE=95187992; PubMed=7882170;

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-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT: HETERODIMER OF AN HEAVY AND A LIGHT CHAINS LINKED BY A DISCHEDING BOND. ALPHA-E ASSOCIATES WITH BETA-7.
-!- SUBCELULAR LOCATION: TYPE I membrane protein.
-!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: Selongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0185; WRPADOMAIN.
SMART; SM00191; Int. alpha; 3.
SWART; SM00327; WWA; 1.
SMART; SM00327; WWA; 1.
SMART; ENSO324; WRFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTEGRIN ALPHA-E.
INTEGRIN ALPHA-E LIGHT CHAIN.
INTEGRIN ALPHA-E HEAVY CHAIN.
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POTENTIAL.
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FG-GAP 2.
X-DOMAIN (EXTRA DOMAIN)
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GFFKR MOTIF.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
PG-GAP 7.
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                                                                                                                                                                                                                                                                                                                                      WGD; MGI:1298377; Itgae.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WWF_A.
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Pfam; PF00357; integrin A; 1.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                 EMBL; U12236; AAC52142.1; -. HSSP; P11215; 1A8X.
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CHAIN
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1083 VVYEKQMLYLYVLSGIGGLLLLLIFIVLYKVGPFKRNLKEKMEAGRGVPNGIP 1136

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                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.

185SUB SPECIFICITY: LEUNOVITES.

DOWAIN: THE INTERIN: LEUNOVITES.

WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

WITH I-DOMAINS TO NOT UNDERGO PROTEASE CLEAVAGE.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 1 WFA domain.

SIMILARITY: Contains 7 FG-GAP repeats.
                             01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last unotation update)
1ntegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (Leukocyte function associated molecule 1, alpha chain)
                                                                                                                       ITGAL OR LFA-1.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                         MEDIINB-91268576; PubMed-2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
alpha-subunit and its expression in COS cells.";
J. Immunol. 147:369-374(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETEROJIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-LASSOCIATES WITH BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSIȚE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWPA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:96606; Itgal.
InterPro: IPRO00413; Integrin_alpha.
InterPro: IPRO00413; INTEGRIN_A.
Pfam: PF001839; PG-GAP; 3.
Pfam: PF001839; Integrin_A; 1.
Pfam: PF00185; INTEGRINA.
PRINTS; PR00185; INTEGRINA.
SMRRT; SM00191; Int_alpha; 5.
SMART; SM00191; Int_alpha; 5.
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HSSP; P20701; 1LFA.
 STANDARD;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI TaxID=10090;
ITAL MOUSE
P24063;
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 IGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSS 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MALRY----LLLTALTL---CHGFNLDTENAMTFQENA-RGFGQSVVQLQGSRVVVGAPQ
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(POTENTIAL).
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                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                            26.0%; Score 1549; DB 1; Length 1163; 34.2%; Pred. No. 5e-95; Live 216; Mismatches 464; Indels 106
                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                SXTRACELLULAR (POTENTIAL)
                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
FG-GAP 1.
FG-GAP 2.
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BY SIMILARITY.

N-LINKED (GLCNA).

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FG-GAP 4.
FG-GAP 5.
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les 409; Conservative 2
Signal; Magnesium; Calcium;
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1163 AA;
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236 SQEGFSAALTSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA 409 409 466 469 524 524 584 581 703 699 753 758 813 867 FRSEKSRQELNTIASKPPRDHVPQVNNFBALKTIQNQLREKIFALEGTQTGSSSSFEHEM 350 GOSLSGGODLIMDGLVDLIVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV - KGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQT 642 NKMKEGVNITICPQI-KSLYPQF-QGRLVANLTYTLQLDGHRTRRRGLFPGGRHELRRNI ONTYLSECYLFRONLOGEPHIOSEPEFOECIKG----NVDLVFLFDGSMSLQPDEFOKIL BFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATG DFWKDVMKKLSNISYQPAAVQPSISYKIEFDPSDYVKRKDPDALLKHVKHMLLLINTFGA IRKVVRELFNITNGARKNAPKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA SSSGISADLSRGHAVVGAVGAVGAKDWAGGFLDLKADLQDDTFIGNEPLTPEVRAGYLGYTVT ::: :: | | :: | | :: | :: | ILIQDQEDSTLYVSFTPKGPKIHQVKHMYQVRIQPSIHDHNIPTLEAVVGVPQPPSEGPI 1040 IQEEFNATLKGNLSPDMYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVE FRQEILVQVIGTLELVGEIEAS-SMFSLCSSLSISFNSSKHFHLYGSNASL-AQVVMKVD ENTYVKGLCPLFGSNIR----QQPQKPPEALRGCPQEDSDIAPLIDGSGSIIPHDFRRMK -IILRNRVQSLVLGAPRYQHIGLVAMFR--QNTGMWESNANVKGTQIGAYFGASLCSVDV DSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAV--LYGEQGQPWGRFGAA HSETWEI-----PPEKNCGEDKKCEANLRVSFSPARSRALRLTAFASLSVELSLSNLEED 814 SYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACES--ASSTEVSGALKSTSCSINHPI :| |: || || || || || || || AYWVQLDLHFPGLSFRVEEN---SCNVSSPI PPENSEVTFNITFDVDSKASLGNKLLLKANVTSENN----MPRTNKTEFQLELPVKYAVY 984 WDRPQVTFSENLSSTCHTK--BRLPSHSD--FLAELRKAPVVNCSIAVCQRIQCDIPFFG : | | : | | : | | THQWSVQMEPPV--PCHYEDLERLPDAAEPCLPGALFRCPVV-----PFEVPNPLPLIVGSSVGGLILLALITAALYKIGPPKRQYKDMMSEG-GPPGAEP 1152 us-09-902-481b-1.rsp

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   SIAVÇQRIQCDIPFFGIQBEFNATLKGNLSFDWYIKTSHNHLLLIVSTABILFNDSVFTLL 1083
                                                                                         1019 SIADCLQPRCDVPSFSVQBELDFTLKGNLSFGWVRBTLQKKVLVVSVABITFDTSVYSQL 1078
RSLPISLVFLVPVRLNOTVIWDRPOVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                               MEDLINE-89139587; PubMed-2537322;
Larzon R.S., Corbi A.L., Berman L., Springer T.;
Primary structure of the lenkocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,
Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,
Pubrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Bichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from
Human chromosome 16p and 16q.";
Genomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214. MEDLINE-96036067; PubMed=7479767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99425288; PubMed=10493852; Kallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G., Cottens S., Weitz-Schmidt G., Hommel U.; "Structural basis for LFR-1 inhibition upon lovastatin binding to the
                                                                                                                                                                                                                                              TTAL HUMAN STANDARD; PRT; 1170 AA.
P20701; 043746;
01-FEB-1991 (Rel. 17, Created)
01-FOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11ntegrin alpha-L precursor (leukocyte adhesion glycoprotein LFA-1 alpha chain) (Leukocyte function associated molecule 1, alpha chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qu A., ieahy D.J.;
"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha
L beta 2) integrin.";
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"The role of the divalent cation in the structure of the I domain from the CD11a/CD18 integrin.";
Structure 4:931-942(1996).
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria; Primates, Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily.";
J. Cell Biol. 108:703-712(1989).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMEL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=No experimental confirmation available;
-: TISSUE SPECIFICITY: LEUKOCYTES.
-: DOMAIN: THE INTEGRIN 1-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH 1-DOMAINS DO NOT UNDERGO PROCTEASE CLEAVAGE.
-: SIMILARITY: Belongs to the integrin alpha chain family.
-: SIMILARITY: Contains 1 VWFA domain.
-: SIMILARITY: Contains 1 VWFA domain.
-: DATABASE: NAME=PROW; NOTE=CD guide CDila entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdila.htm".
                               FUNCTION: INTEGRIN ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAMI, ICAMI, ICAMI, ICAMI ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAMI, ICAMI, ICAMI AND ICAMI. IT IS INVOLVED IN A VARIETY OF IMMUNE PHENOMENA INCLUDING LEUKOCYTE-ENDOTHELIAL CELL INTERACTION, CYTOTOXIC T-CELL MEDIATED KILLING, AND ANTIBODY DEPENDENT KILLING BY GRANULOCYTES AND MONOCYTES.
                                                                                                                                                                                                        -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-L. ASSOLTATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Signal; 3D-structure; Magnesium; Calcium; Repeat;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
FG-GAP 2.
VWFA.
                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P20701-2; Sequence=VSP_002738;
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GO; GO:0006928; P:cell motility; TAS.
InterPro; IPRO00413; Integrin_alpha.
InterPro; IPRO02035; VWF A.
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PROSITE; PS50234; VWPA; 1.
Integrin; Cell adhesion; Receptor; G
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EMBL; AC002310; AAC31672.1; -.
PIR; S03308; S03308.
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Pfam; PF00357; integrin A; 1.
Pfam; PF00092; vwa; 1.
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PRINTS; PR00483; VWFADOMAIN.
SWART; SW00191; Int_alpha; 4.
SWART; SW00327; VWA; 1.
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MIM; 153370; -.
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PDB, 1ZOP, 07-DEC-96
PDB, 1CQP, 07-AUG-00.
PDB, 1DGQ, 03-FBB-00.
PDB, 1MJN, 28-JAN-03.
PDB, 1MQ9, 14-JAN-03.
PDB, 1MQ9, 14-JAN-03.
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07-DEC-96.
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07-AUG-00.
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CD11a I-domain.";
J. Mol. Biol. 292
-!- FUNCTION: INT
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365 PLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVLGAP 424
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                                                                                                                                                                                                                                                                                                                                 125 LPGSNIRQQPQXPPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                   305 SKPPRDHVFQVNNFBALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGP 364
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   .) (POTENTIAL)
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                                                                                                                                 Length 1162;
N-LINKED (GLCNAC. . .) (POTEN
N-LINKED (GLCNAC. . .) (POTEN
MISSING (IN REF. 2)
GHPW -> ATP (IN REF. 2)
L -> V (IN REF. 2)
V -> A (IN REF. 2)
S MW, F296AlA35455D77D CRC64;
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58.0%; Score 3455; DB 1;
Best Local Similarity 59.9%; Pred. No. 4.4e-222;
Matches 684; Conservative 162; Mismatches 287;
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          MIMI, 602453; ---

MIMI, 602453; ---

R GO; GO:0008305; C:integrin complex; TAS.

R GO; GO:0004895; F:cell adhesion receptor activity; TAS.

R GO; GO:001637; P:cell-cell adhesion; NAS.

R GO; GO:000055; P:cell-cell adhesion; NAS.

R GO; GO:000055; P:manne respone; NAS.

R InterPro; IPR00043; Integrin_alpha.

R InterPro; IPR00043; Integrin_alpha.

R Pfam; PF00183; PRG-GAP; 3.

Pfam; PF00183; WR-A.

PRINTS; PR01185; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R RAART; SM00191; Int_alpha; 4.

SMART; SM00327; WWA-1.

R RAART; SM00327; WWA-1.

R RAART; SM00327; WWA-1.

R RAART; CASCOLAL; WWA-1.

R RAART; CASCOLAL; WWA-1.

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M SAART; CASCOLAL; WA-1.
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(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
     SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 1 VWPA domain. SIMILARITY: Contains 7 FG-GAP repeats.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U40274; AAB60634.1; -...
EMBL; U40275; AAB60635.1; -...
EMBL; U40277; AAB60635.1; -...
EMBL; U40277; AAB60637.1; -...
EMBL; U40279; AAB60638.1; -...
EMBL; U40279; AAB60638.1; -...
EMBL; AF187881; AAF62875.1; -...
HSSP; P11215; 1A8X.
Genew; HGNC: 6146; ITGAD.
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LLLFTALATSLGFNLDTBELTAFRVDSAGFGDSVVQYANSWVVVGAPQX1TAANQTGGLY
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ASSOCIATES WITH BETA-2.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! TISSUE SPECIPICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL.

LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.

-!- DOWAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN: INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a human
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INTERACTION WITH VCAMI.

MEDLINE-99059812; PubMed-9841932;
Grayson M.H., Van Geral M., Sterbinsky S.A., Michael Gallatin W., Grayson M.H., Van Geral D.E., Bochner B.S.;
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the leukocyte integrin
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Van der Victen M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Van der Victen M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.,
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
binding interface between I domain and VCAM-1.";
J. Immunol. 163:1984-1990(1999).
J. Immunol. 163:1984-1990(1999).
J. Immunol. 163:1984-1990(1999).
J. CAMI. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS
CLEARING LIPOPROTEINS PROM PLAQUES AND IN PHAGOCYTOSIS OF BLOOD
BORNE PARHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
                                                                                                                                                                                                                                                                                                                                                                                                             St John T.,
                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel leukointegrin, alpha d beta 2, binds preferentially to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJURE 96257236; PubMed=8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; Coning and chromosomal localization of a novel gene-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910-1125
                                                                                                                                                                                                                                                                                                                                                                                                         Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., Staunton D.B., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
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                                                                                                                 THUMAN STANDARD; FAL, TAIN STANDARD; G13349; Q15575; Q15576; G15-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 467-537; 571-602; 633-666;
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MEDLINE=96111956; PubMed=8777714;
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Gene 171:291-294 (1996).
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Genew; HGNC:6152; ITGAX.
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                   FALLPGGESYVRSKTETKVEPYEVHNPVPLIVGSSIGGLVLLALITAGLYKLGFFKRQYK 1139
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1080 FILLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYK 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and p150,95 leukocyte adhesion proteins.";

J. Immunol. 138:2381-2383 (1997)

-!- FUNCTION: INTEGRIN ALPHA-X/BETA-2 IS A RECEPTOR FOR FIERINOGEN. IT RECOGNIZES THE SEQUENCE G-P-R IN FIBRINOGEN. IT MEDIATES CELL-CELL INTERACTION DURING INFLAMATOR RESPONSES. IT IS ESPECIALLY INFORMATION TO DURING INFLAMATOR RESPONSES.
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X ASSOCIATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- INSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRANDLOCYTES.

DOWAIN: THE INTEGREN I-DOWAIN (INSERT) IS A VWFA DOWAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 1 VWFA domain.

SIMILARITY: Contains 7 FG-GAP repeats

DATABASE: NAME-SFOW; NOTE=CD guide CD11c entry;

WWW.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=8816645; PubMed=3327687;

Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;

"cDha cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95.";

EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                            01-FBE.1991 (Rel. 17, Created)
01-FBE.1991 (Rel. 17, Last sequence update)
01-FBE.1991 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation u
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MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte
p150, 95 molecule.";
J. Biol. Chem. 265:2782-2788(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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Best Local Similarity 61.3%; Pred. No. 2.8e-225;
Matches 700; Conservative 138; Mismatches 297;
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EMBL, M81695, AAA59180.1; -.
EMBL, Y00093; CAA8283.1; -.
EMBL, M29485, -, NOT_ANOTATED CDS.
EMBL, M29487; AAA51620.1; ALT SEQ.
EMBL, M29482; AAA51620.1; JOINED.
EMBL, M29484; AAA51620.1; JOINED.
EMBL, M29484; AAA51620.1; JOINED.
EMBL, M29485; AAA51620.1; JOINED.
PMR, A3684; RWHUIC.
PDB, 1N3Y; 18-FEB-03.
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R EMBL; M14293; AAA39484.1; -

R EMBL; M14293; AAA39484.1; -

R EMBL; M1292; S00551.

R EMSP; P1215; AAAX.

R DIAMS; P1215; AAAX.

R InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR00235; VWP_A.

R Pfam; PF00357; integrin_A; 1.

R Pfam; PF00357; integrin_A; 1.

R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR00453; VWFADCMAIN.

R SWART; SM00191; Int_alpha; 5.

R SWART; SM00191; Int_alpha; 5.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.

Integrin, Cell adhesion; Receptor; Glycoprotein; Transmembrane;

X SIGNAL: 16
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SIMILARITY: Contains 1 VWFA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
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MEDLINE=88312584; PubMed=3044779;
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0; Mismatches
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Best Local Similarity 99.9
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ADHESIVE INTEGRATIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES
AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COATED PARTICLES.
IT IS IDENTICAL WITH CR. THE RECEPTOR FOR THE ICI3S FRAGMENT OF
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D
FEPTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR
FIRSINOGEN FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES
OF FIRSINOGEN GAMA CHAIN. ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN
MAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-WEDIATED
GLOMBENTINES MICE EXPRESSING A NULL WITATION OF THE ALPHA-M
SUBBNIT GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMULATION, IN
RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
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VNCSIAVCQRIQCDIPPFGIQEEFNATLKGNISFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                      1080 TILPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
                                                           TLLPGQGAPVRSQTETKVBPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGPPKRQYKD
                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (Rel. 09, Created)
01-FRB-1991 (Rel. 17, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
1ntegrin alpha-M precureor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
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STRAIN=BALB/C; TISSUE-Spleen;
MEDLINE=86287312; PubMed=2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.B.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85188276; PubMed-3887182;
Springer T.A., Teplow D.B., Dreyer W.J.;
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
glycoproteins and unexpected relation to leukocyte interferon.";
Nature 314:540-542(1985).
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with the integrin family and an additional domain reveals. Willebrand factor."; EMBO J. 7:1371-1378(1988).
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the Buropean Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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PRINTS; PRO045; VWFADOMAIN.
SMART; SM00191; Int. alpha; 4.
PROSITE; PS00242; VMFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VMFA; 1.
PROSITE; PS50234; VMFA; 1.
PROFITE; 
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GO; GO:0004895; F:cell adhesion receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
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BMBL; M18044; AAAS9491.1; -.
BMBL; J04145; AAAS9903.1; -.
BMBL; S52127; AAB24821.1; -.
BMBL; S52152; AAB24821.1; JOINE
BMBL; S52152; AAB24821.1; JOINE
BMBL; S52153; AAB24821.1; JOINE
BMBL; S52155; AAB24821.1; JOINE
BMBL; S52155; AAB24821.1; JOINE
BMBL; S52155; AAB24821.1; JOINE
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Pfam, PF00357, integrin_A, 1.
Pfam, PF00092, vwa, 1.
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AAA58410.1;
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PDB; 1BHO; 18-NOV-98.
PDB; 1IDN; 25-NOV-98.
PDB; 1IDN; 01-AUG-96.
PDB; 1IDN; 07-AUG-96.
PDB; 1IMI; 07-AUG-97.
PDB; 1MIU; 07-AUG-97.
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1A8X; 17-JUN-98.
1BHO; 18-NOV-98.
1BHQ; 18-NOV-98.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration
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ACTION OF C., Springer T.A.; Stringer T.A.; Str
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SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains I VMFA domain.
SIMILARITY: Contains I PG-GAP repeats.
DATABASE: NAME=PROW, NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl1b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin
CR3 (CD118)/CD18).";
CR1 80:631-638(1995).
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MEDLINE=5633671; PubMed=8747460;
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"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE=98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbarks W.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
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                           MEDLINE=92073318; PubMed=1683702; Shelley C.S., Arnaout M.A.; "The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression."; Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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mus musculu	mus musculu	drosophila	homo sapien	nomo sapien	cavia porce	caenorhabdi	homo sapien	rattus norv	caenorhabdi	drosophila	drosophila
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ITA7_MOUSE	ITAB MOUSE	ITA1 DROME	ITAB HUMAN	ITA8 HUMAN	ITAM CAVPO	PAT2 CABEL	ITA7 HUMAN	ITA7 RAT	INA1 CABEL	ITA3 DROME	ITAS_DROME
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ALIGNMENTS

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MEDINE=88190151; PubMed=2833753; Arnaout M.A., Harris P., Tenen D.G., Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G., "Molecular cloning of the alpha subunit of human and guinea pig leukccyte adhesion glycoprotein thromosomal localization and homology to the alpha subunits of integrine."; Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLINE=88257215; PubMed=2454931;
ARIBOLINE=88257215; PubMed=2454931;
ARIBOLINE=88257215; PubMed=2454931;
ARIBOLINE=88257215; PubMed=2454931;
ARIBOLINE=8827215 adhesion receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                               01-37L-1989 (Rel. 11, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11ntegrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor).
1TGAM OR CR3A OR CD11B.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
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                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE=88315033; PubMed=2457584;
MEDILINE=88315033; PubMed=2457584;
MEDILINE=88315033; PubMed=2457584;
MIDILINE=88315033; PubMed=2457584;
MIDILINE HIGH T.A., Miller L.J., Springer T.A.;
The human leukocyte adhesion glycoprotein Mac-1 (complement recetype 3, CD11b) alpha subunit. Cloning, primary structure, and tration to the integrins, von Willebrand factor and factor B.";
MEDIL Chem. 263:12403-12411(1988).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 9-1153 FROM N.A.
MEDLINE-89098893; PubMed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
1152 AA
    PRT;
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    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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    ITAM HUMAN
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ENYLPDHIDISYTVTVDSGIIANRRAMFVDNDMSEITKTRRLAVSTQFCDPLRAY 557

/IMDRPQ------VTFSENLSSTCHTKERLPSESDFLAELRKAPVV 1021 CORIOCDIPFFGIQEFNAT ----LKGNLSFDWYIKTSHNHLLIVSTAEILF 1075 :LLPGQGAFVRSQTETKVE--PFEVPNP--------LP----- 1108 ICODDLSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSY 829 IRPYFKARSENS--EDPNTLENNELNMTVPVTVDCTLKLLSASYPEIVMYSTQED 775 IDPVSPIVLRINFSIVGTPLSAFGN------LRPVLAEDAQRLFTALFPFEK 769 ONORSORSWRLACESASSTEVSGALKSTSCSINHPIFPEN----SEVTFNIT 883 ----KASLGNKLLLKANVTSBNNMPRTNKTBFQLELPVKYAVYMVVTSHGVSTK 938 ---NFTASENTSRVMQHQYQV----SNLGQRSLPIS----LVFLVPV 976 SSVGGLLLLALITAALYKLGFFKR-----QYKDMMS--EGGPP 1148

Search completed: June 7, 2004, 17:17:33 Job time : 20.7639 seca

Tue Jun

us-09-902-481b-1.rpr

Db 974 H	RESULT 14 158409 integrin alpha-	C;Species: Homo C;Date: 02-Jul- C;Accession: I5 R;Hibi, K.; Yam	Oncogene 9, 611 A;Title: Aberra A;Reference numl A;Accession: IS:	A;Status: preli A;Molecule type A;Residues: 1-1. A;Cross-referen	R;Palmer, B.L.; J. Cell Biol. 1: A;Title: Sequen A;Reference numl	A,Accession: A4. A,Status: prelin A,Wolecule type A,Residues: 30-	A;Cross-reteren C;Superfamily: C;Keywords: gly: F;1-27/Domain:	Query Match Best Local Sir Matches 237;	Oy 347 E3	Oy 406 YI Db 249 YI	Qy 462 CS	Oy 522 GJ Db 365 GI	Qy 582 Q) : Db 424 RM	Cy 640 NI :- Db 483 HI	Qy 692 F- Db 532 F1	Oy 745 AF	794	
	172 FVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGI 231	232 RKVVRELFNITNGAR-KNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA 290 	291 FRSEKSRQELNTIASKPPRDHVPQV-NNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHE 349 175PPDLRTELSKRIAPCYQDYVKKFGENFAS	350 MSQEGPSAALTSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGY 406	OIGAYPGAS 4 :: : KLGSYPGAS 3	461 LCSVDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPLPRGORARWQC-DAVLYGEQGQPWG 519 : : ::: :	520 REGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSP 579 :: :	580 RLQYPGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMERNPREVARNVF 637	638 ECNDQVVKGKEAGEVRVCL4VQKSTRDRLREGQIQSVVTVDLALDSGRPHSRAVF 692	693 NETRNSTRROTOVLGLIQUCETLKLOLPNCIEDPVSPIVLRINPSLVGTPLSAFG 747 9 :	748 NLRPVLAEDAQR-LFTALFPEKNCGNDNICQDDLSITFSFMSLDCLVVGGFRE 800 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	801 FNVTVTVRNDGEDSYRTQVTFFFFLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGAL 860	861 KSTSCSINHPIPPENSEVTENITFDVDSKASLGNKLLKANVTSEN-NMPRINKTBFQL 918 : : : : : : : :	919 ELPUKYAVYMVVTSHGVSTKXLNFTASENTSRVMQHQYQVSNLGQRSLF-ISLVF 972 	973 LVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIA 1026 	1627 VCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFN 1076		1107
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.-9 chain precursor - numa...
.-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2000
.-1896 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2000
IS8409; A49459
amakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Taka
anakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Taka
11-619, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ant upregulation of a novel integrin alpha subunit gene at 3p21.3 in smalmber: IS8409; MUID:94119603; PMID:6290272
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be: mRNA
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1205 -RES3
1205 
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imilarity 26.5%; Pred. No. 3.3e-35;
; Conservative 160; Mismatches 332; Indels 164; Gaps
HHQRPKRYFTIVIISSSLLLGLIVLLLISYVMWKAGFFKRQYKSILQE 1021
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integrin alpha-4 chain
ycoprotein; metal binding; transmembrane protein
signal sequence #status predicted <SIG>
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------CQAGISSFYTQDLIVWGAPGSSYWTGTVFVYNITTNQYKAFVD--R 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 VDSDWNDAYLGYA--AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV---- 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVVDA--QGHVLLLRSQPVLRVKAIM 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGR 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-HPESVNRTKPDCT-----ENGLPSVCMHLTLCFSYKGKEVPGYIVLFYNVSLDVHR 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---PHSRAVF--NETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSL-- 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 KAESPERPYFFSNGTSDVITGSIRVSSSGEKCRTHQAFMRKDVRDILITPIHVEATYHLGH 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VGTPLSAFGNLRPVLAEDAQR-LFTALFPFEKNCGNDNICQDDLSITFS----FM 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 GTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLY--TSKEKSTFINMTR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 ONOVKFGSYLGYSVGAGHFRSPHTTEVVGGAPQHEQIGKAYIF----SIDENELNIVYEM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRA-RWQCD 507
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                                                                                                                                                 2 ALRVILLTALTLCHGFNLDTENAMTRQ-ENARGRGOSVV-QLQGSR--VVVGAPQEIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------RKFGB------
                                                                                                                                                                                                                    58 N----ORGSLYQCDYSTG---SCEPIRLQVP------VEAVNMSLGLSLAATTSP-
A, Residues: 1-1039 <NEU>
A, Cross-references: EMBL-X51176, NID:951484; PIDN:CAA37316.1; PID:951485
C, Superfamily: integrin alpha-4 chain
C; Keywords: cytoskeleton; transmembrane protein
                                                                               tch 11.2%; Score 667; DB 2; Length 1039; al Similarity 22.6%; Pred. No. 8.9e-38; 284; Conservative 190; Mismatches 412; Indels 368;
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Best Local Similarity
Matches 284; Conserv
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A;Accession: A33355
A;Molecule type: DNA
A;Residues: 1-93 a ROS-
A;Residues: 1-93 a ROS-
A;Cross-references: GB:M62841
B;Talkada, Y:, Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A;Title: The very late antigen family of heterodimers is part of a superfamily of molec A;Reference number: A94151; MUID:87204112; PMID:3033641
A;Accession: D28018
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A;Rebidues: 1-1038 TRK.
A;Cross-references: GB:X16983; EMBL:X15356; NID:g33945; PIDN:CAA34852.1; PID:g33946
R;Rosen, G.D.; Birkenmeier, T.M.; Dean, D.C.
Proc. Natl.: Acad. Sci. U.S.A. 88, 4094-4098, 1991
A;Tille: Characterization of the alpha-4 integrin gene promoter.
A;Reference number: A39355; MUID:91239513; PMID:2034655
                                                                                             1003
                                                                                                                                                                                           1004 --RLPSHSDFLAELRKAPVVNCSIA--VCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIK 1059
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                                                                                                                                            876
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                         112 TCSENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKE 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrin alpha-4 chain precursor - human
NiAlternate names: CD49d; very late antigen-4 alpha chain; VLA-4 alpha chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Staces: O1-Dec-1989 #text_change 24-Sep-1999
C;Accession: S06046; A39355; D28018
C;Accession: S06046; A39355; D28018
C;Accession: S06046; A39356; D28018
C;Accession: S06046; MUID:89356603; PMID:2788572
A;Accession: S06046; MUID:89356603; PMID:2788572
                                                                                                                                                                                                                                                                                                                          NMPRINKTEPQLELPVKYAVYMVTSHGV--STKYLNFTASENTSRVMQHQ----YQVS
                                                                                                                       820 NTGISMADNVSVKIMVP---NSPLPQDDKLFNVLDVQTTTGQCHFKHYGRECTFAQQKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: cell adhesion; cytoskeleton; duplication; glycoprotein; hete
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-1038/Product: integrin VLA-4 alpha-4 chain #status predicted <MAT>
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                                                                                                                                                                                                                          NIGORSLP-ISLVFLVPVRLNQTVIWDRP--QVTFSENLSSTCHTKE--
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C, Superfamily: integrin alpha-4 chain
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OY 911 TNKTEFQLELEVKYAVYMVTSHGVSTKYLNFTASENTSRVMCHQTQVSNLGQR 964 Db 921 KADNLVNLKIPLLYDAEIHLTRSTNINFYEISSDGNVPSIVHSFEDVGPKFIFSLK 976 QY 965SLPISLVPLV	459 ASLCSVDVDSNGSTDLVLIGAPHYYEQTR-GGQUSVFG 490 459 ASLCSVDVDSNGSTDLVLIGAPHYYEQTR-GGQUSVCPLPRGQRA 502 1
ુ મુખ માને મેને મેને મેને મેને મેને મેને મેને	Db 723 VTLDSLRQISRSFPSGTQERKIQNITVRESE
112 FUSEVITY VALICE LEGS NUMBER OF A LANGE OF GENERAL STREET OF ST	Db 1124

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F;172-347/Domain: von Willebrand factor type A repeat homology <wwa2> F;1134-1154/Domain: transmembrane fletatus predicted <twa> F;1154-1154/Domain: intracellular fletatus predicted <twa> F;1155-1181/Domain: intracellular fletatus predicted <twa> F;1157-1181/Domain: intracellular fletatus predicted <twa> F;105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (con Query Match Best Local Similarity 27.3%; Pred. No. 6.2e-67; Matches 339; Conservative 214; Mismatches 498; Indels 193; Gaps 44; OY 1. INTLATALTALCHGFNLDTENAMTFQ-ENARGFGOSVVQLCGSRVVVGAPQE 53 </twa></twa></twa></twa></wwa2>	105 105 131 165 169 223 247 247 306	337 GTOTGSESSEPHENSGEDERALITERITATION TO THE STATEMENT OF
CY 742 PLSAFGNIAPULABDAQRIATALPPPEKNCCNDNICODDISITRSEMSIDC 792 : :	Qy 965SLPISLVFLV	RESULT 10 MALEATRACE AND ADDRESS CRAIN PRECURSOR - Human WALEATRACE AND ADDRESS CRAIN CSPECIES: Romo sapismes (Can) MATTLE The primary structure of the VLA-2/collagen receptor alpha(2)-subunit (platelet A; Reference number: A3398; MUD:89308879; PMID:2545729 A; Molecule type: Romo sapismes A; Residues: 1188 - Ramentier, S.; Leug, L.L.; McGregor, J.L. Biochem. J. 279, 419-425, 1994 A; Molecule type: protein A; Reference number: A56793; MUD:92061944; PMID:1953640 A; Molecule sapismes (GPIC, GPIC,

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STAEI-LFNDSVFTL-----LPGQGAFVRSQIETKVRPPE-VPNPLPLIVGSSVGGLLL 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYLGYSVARISTGNSVHFVAGAPRANYTGQIVLYSVN----ENGNVTVIQSQRGDQIGS 478
                                                                                                                                                                                                                                                                                                                                            SRGLFKENNERCLQXTMIVSQAQRCSEYIIHIQEPS---DIISPLANLCMVISLENPGT-- 756
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                                                                                                                                                                                                                                                                                QGQPWGRFGAALIVLGDVNGDKLTDVAIGAPGBEDNRGAVYLFHGTSGSGISPSHSQRIA 573
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 231
                                                                                                                                        EHEMSQEGFSAAIT--SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-D 401
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             YFGSVLCAVDVNXDTITDVLLVGAPMYMNDLKKEEGRVYLFTITKG-ILNWH--QFLEGP
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                                                                                           -GDAFRSEKSROBLNTIASKPPRDHVFQVNNFEALKTIQNQLREKIFALEGTQTGSSSSF
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EQLK--KSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLL----GRTHTATGI
                                              rkvvrelfnitngarknafkilvvitdgekfgdplgyedvipeadregviryvigv-
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Cybace: 12-can-12-3 medyweinc_1erresson. 2 condera, H.; Wang, D.Z.; Damjanovich, L.; Lat; Stelman, J.M.; Chan, B.M.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Lat; submitted to the EMBL Data Library, January 1994
A; Reference number: S44142
A; Accession: S44142
A; Accession: S44142
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1178 cBDS
A; Residues: 1-1178 cBDS
A; Cross-references: EMBL: 229987; MID: G473099; PIDN: CAA82877. 1; PID: G473099
F;169-344/Domain: von Willebrand factor type A repeat homology <VWA2>
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VLA-2 protein homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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652 KVNIQKKNCHMEGKETVCINATVCFEVKLKSKEDTIYEADLQYRVTLDSLRQI 70. 688 SRAVFNETKNSTRRQTQVLGLTQTCETLXLQLPNCIEDPVSPIVLRLNFSLVGT 74.	DD 705 SRSFEGTQERKVQRNITVRKSECTKHSFYMLDKHDFQDSVR 742 PLSAFGHIRPVLAEDAQRLFTALPPFEKNCGNDNICQDDLSITFSFMSL 756 PENGPVLDDSLPNSVHSTIPFAKDCGNKEKCISDLSHAYTTEK QY 801 FNVTVTVRNICAEDSYRTOVTFPPLDLSYKKVSTLQNQRSQRSWHACE	RESULT 8 integrin alpha 2 subunit - bovine (fragment) C;Species: Bos prinigenius taurus (catt.e) C;Accession: 145914 N;Takeda, Y: J. Biol. Chem. 269, 9659-9663, 1994 A;Title: Identification of putative ligand binding sites within the I-domain of integrin A;Recterace number: A54402; MUD:94139647; PMID:7511592 A;Accession: 145914 A;Accession: 145914 A;Accession: 145914 A;Molecule type: mRWA A;Rectule : preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRWA A;Rectules: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRWA A;Restuloral Similarity 27:84; Score 1099; DB 2; Length 1170; Best Local Similarity 27:84; Pred. No. 9.66-68; Matches 340; Conservative 215; Mismatches 498; Indels 168; Gaps 47; April 1 LTCHGPNLDTENAMPED-ENARGFORSYNONFUNPKONFULVORSPYRYC 72 A; IL LTCHGPNLDTENAMPED-ENARGFORSYNONFUNPKONFULVORSPYRYC 72 A; G7 - LYSTGOSCEPIRLO
Oy 1107 LPLIVGSSVGGLLILALITAALYKLGFFKRQYKDMWSB 1144 : : : : :	RESULT 7 #45126 integrin alpha-1 chain - human (fragment) C.Species: Homo sapiens (man) C.Species: Homo sapiens C.Speci	09 182 -KSKTLFSLAMOYSBEPRIHFTFKEFORNURPRSLUKPITOLIGR-THTATGIRKUVRRELF 239 175 GPROTOVGIVOYGENVTHEPILAKTSTEEVLVAARKI

64 PGPLHRCSLVQDEILCHPVEHVPIPKGRHRGVTVVRSHHGVLICIQVLVRRPH 116 111 QTCSENTYVKGLCFLFGSNLRQQPQ		136 -KFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWGEFVSTWMEQL- 180 174 ARQREALEKEBEDKEEEDEBEBERATELIDGSGSIDPPDFDRAKDFISRWRNFY 233	-KKSKTLFSLMQYSBEFRIHFTFKBFQNNPNPRSLVKDITQLLGRTHTATGIRKVVRELF	234 EKCFECNPALVQYGGVIQTEPDLRDSQDVMASLARVQNITQVGGVTKTASAMQHVLDSIF 293 240 NITNGARKNAPKILVVITDGEKFGDPLGYEDVIPBADREGVIRYVIGVGDAFRSEKSRQE 299	294 TSSHGSRRKASKVMVVLTDGGIFEDPLNLTTVINSPKMQGVERFAIGVGEBFKSARTARE 353 300 LNTIASKPPRDHVPQVNNFBALKTIQNQLREKIFAIEGTQTGSSSSFFHEMSQEGFSAAI 359	:::: ::: :::		TCSLSYVAGAPQYKHHGAVFELQXEGREASFLPVLEGEQ@GSYFGSELCPVDIDMDGS TDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARMQCDAVLXGEQQQPWGRFGAALTVLGDV			646 GKBAGGFDISGDGLADITYGTLGQAVVFRSRPVYRLKVSNAFTPSALPIG 696 646 GKBAGGVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNBTKNSTRRQTQV 705	LGLTQTCETLKLQLPNCIEDPVSPIVLRLMFSLVGTPLSARGNLRFVLAEDAQRLF	762 TALPPFERNCGNDNICQDDLSITPSFMSLDCLAVGGPREFNVTVTVFNDGEDSYRTQVTF 821	822 FFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFN 881	882 ITFDVDSKASLGNKLLLKANVTSERAMPRTNKTEFQLELPVKXAVYMVVTSHG 934 : : :	935 VSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFS 992	993 BNLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNL 1052 : : : : : :	1053 SPDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNP 1106
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OY S81 LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVPECN 640 ::: : : :	641 DQVVKGKEAG-EVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNST	Db 636 YSAREEQKHGYKLKACPRIKDLTPQPQGRLILANLSYTLQLDGHRWRSRGLFPDGSHBL 693 Qy 700 RRQTQVLGLTQFCGTLKLQLPNCIEDPVSPIVLRINPSLVGTPLSAFGN-LRPVLAB 755	694 SGNTSITP-DKSCLDFHFHFPICIQDLISPINVSLNFSLLEBEGTPRDOKGRAMQPILRP	Qy 756 DAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTN 809 :	QY 810 DGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGAL-KSTSCSIN 868	Qy 869 HPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSEN-NMPRTNKTEPQLELPVKYAVY 927			QY 1039 GIQEEPNATLKGNLSPDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTETKV 1098 DD 1022RWEILIQVTGTVELSKEIKAS-STLSLCSSLSVSFNSSKHFHLYGSKA-SEAQVLVKV 1077	Qy 1099 EPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM-SEGGPPGAEP 1152 :	RESULT 6 A3213 integrin alpha-E chain - human C.Species: Homo sapiens (man)	r, c.M.	Ajitis: Nojectiar tioning of the numan mucosal lymphocyte integrin alpha(s) subunit, un Ajitis: Nojection A53213, MUID:94164962, PMID:8119947 Ajacession: A53213 Ajacession: Preliminary Ajacession: A53213	A;Nolecules Lype: mkwh A;Residues: 1-1179 <sha> A;Cross-references: GB:L25851; NID:g457244; PID:g457245</sha>	A;Cross-references: GDB:330801 A;Gross-references: GDB:330801 A;Map position: 17p13 C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo F;199-371/Domain: von Willebrand factor type A repeat homology <vwa3></vwa3>	Query Match 19.5%; Score 1163; DB 2; Length 1179; Best Local Similarity 28.8%; Pred. No. 3.4e-72; Matches 356; Conservative 221; Mismatches 481; Indels 180; Gaps 41;	CHGENLDTENAMTFQENARGFGOSVVOLGGSRVVVGAPQETVAANQ 5	60 RGSLYQCDYSTGSCEPI-RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVH

Oy 1040 IQBENATLKGALSFDWYK	RESULT 5 156126 1Vmphocyte fuction-associated mole lymphocyte fuction-associated mole C;Species: Mus musculus (house mou C;Stecies: Mus musculus (house mou C;Stecies: 26-Jul.1996 #sequence_revice: 26-Jul.1996 #sequence_revice: 26-Jul.1996 #sequence_revice: 156126 R;Kaufmann, Y:; Tseng, E.; Springe Jym A;Faterence number: 156126; MuID:9 A;Accession: 156126 A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1163 ARES> A;Coss-references: GB:M60778; NID C;Genetics: 26-Jul.1163 A;Aenes: 1-1163 A;Aenes: 1-11	C;Superianily: Cell Bullace glycup P;151-315/Domain: von Wilebrand f Query Match Ast Local Similarity 34.2%; Matches 409; Conservative 216 Qy 1 MALRVLLLTALTL Db 1 MSFRIAGPRILLIGLQLFAK	53 60 113 113	173 176 232 236 236	OY 285 IGVGDARKSERNINIA Db 282 IGIGKHFVSVOKQKTLHIPA OY 345 SFBHENSOBGFSAAITSNGP Db 342 SFNMELSSSGISADLSKGHA	Oy 404 LGYAAA-IILRNRVQSLVLG
6 LILITALTICHGFNLDTENAMTFQENARGFGOSVVOLOGSRVVVGAPQEI 54 : : :	115 ENTYVKGLCFLFGSNLRQOPQKFPBALRGCPQEDSDIAPLIDGSGSIIPHDFRRMK 170	350 SSSGISADLSRGHAVGAVGAKDWAGGFLDLADLODDTFIGNBPLTERBAGGTTVT 409 410 **LILRNRVQSLVLGAPRYCHIGLVAMFRCNTGAWESNAMVKGTOLGAYFGASLGSVDV 466	LTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPRLQYF	-KGKEAGEVRVCLHVQKSTRDELREGGIQSVYTYDLALDSGRPHSRAVPNETKNSTRRYT	754 ABDAQRIETALPPEKKOGNONICQDDISITSEMSLDCLVVGGPRERVYVVVTOEDB B13 1 : : :	872 FPENSEVTFNITPDVDSKASLGNKTLLKANVTSENNMPRINKTEFQLELPVKYAVY 927
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protein CD11b, von Willebrand factor type A repeat hom
factor type A repeat homology <VWAl>
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:91268576; PMID:2051027
KTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTBTKVE 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: ||: |||||| :: ||: ||HAVVGAVGAXDWAGGFLDLREDLQGATFVGQEPLTSDVRGGY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAPRYCHIGLVAMFR--ONTGMWESNANVKGTQIGAYFGAS 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CHGFNLDTENAMTFOENA-RGFGOSVVQLQGSRVVVGAPQ 52
                                                                                                                                                                                                                                                    rision 26-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1549; DB 2; Length 1163;
Pred. No. 4.7e-99;
6; Mismatches 464; Indels 106; Gaps
                                                                          JILIALITAALYKIGFFKRQYKDMMSEG-GPPGAEP 1152
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A;Gene: GDB:ITGAL, CD11A
A;Cross-references: GDB:119757; OMIM:153370
A;Map position: 16pl1.2-16pl1.2
C;Superfamily: cell surface glycoprotein CD11b, von Willebrand factor type A repeat h C;Superfamily: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; E;1-2-5,Domain: signal sequence #status predicted <s16.
E;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicte F;154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-170 < LAR>
A; Cross-references: EMBL:Y00796; NID:g31421; PIDN:CAA68747.1; PID:g31422
A; Cross-references: EMBL:Y00796; NID:g31421; PIDN:CAA68747.1; PID:g31422
A; Note: part of this sequence was confirmed by protein sequencing
B; Cornwell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A; Title: Description of the leukocyte function-associated antigen 1 (LPA-1 or CD11a)
A; Reference number: A47458; MUD:93248261; PMID:8097887
A; Accession: A47458
A; Molecule type: DNA
A; Residues: 1-20 < COR>
A; Molecule type: DNA
A; Residues: 1-20 < COR>
A; Molecule type: DNA
A; Residues: C.S.; Farchtzadd (O.C.; Armaout, MA.)
B; Balley, C.S.; Farchtzadd (O.C.; Armaout, MA.)
B; Balley, C.S.; Farchtzadd (O.C.; Armaout, MA.)
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A; Title: Identification of cell-specific and developmentally regulated nuclear facto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secure alycoprotein CD11a precursor - human
N;Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte;
S;Species: Bomo sapiens man)
C;Species: 18-Feb-1990 #sequence revision 28-Feb-1990 #text_change 20-Aug-1999
C;Accession: S03308; A47458; A47565; A48759; S36044
R;Larson, R.S.; Corbi, A.L.; Berman, b.; Springer, T.
J. Call Biol. 108, 703-712, 1989
A;Title: Primary structure of the leukocyte function-associated molecule-1 alpha A;Reference number: S03308; MUID:89139587; PMID:2537322
                                                                                                                                                                                      SIAVCQRIQCDIPFFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL 1083
                                                                                                                                                                                                                                                                                     1084 PGQGAFVRSQTETKVEPFEVPNPLFLIVGSSVGGLLLLALITAALYKIGPFKRQYKDMMS 1143
                                                                                                                                                                                                                                                                                                                RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023
     A, Accession: A47565
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: CAHE
A, Cross-references: GB: M95609
B, Nucda, A,; Lopez-Cabrera, M; Vara, A.; Corbi, A.L.
Biol. Chem. 268, 19305-19311, 1993
A, Title: Characterization of the CD11a (alphal, LFA-lalpha) integrin gene
A, Reference number: A48759; MUID:93374910; PMID:8103515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
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Matches 410; Conserv
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A;Molecule type: DNA
A;Residues: 1-20 <NUE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTRGGQVSVCPLPRGWR-RWWCDAVLYGEQGHPWGRFGAALTVLGDVNGDXLTDVV1GAP
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CDIC #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;149-319/Domain: extracellular #status predicted <TMY>
F;1108-1133/Domain: transmembrane #status predicted <TMY>
F;1184-1163/Domain: intracellular #status predicted <IXT>
F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                       VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY
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9
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Best Local Similarity 61.4%; Pred. No. 1.1e-235;
Matches 701; Conservative 138; Mismatches 296;
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A,Gene: GDB:ITGAX, CD11C
A,Cross-references: GDB:119758; OMIM:151510
A,Cross-references: GDB:119758; OMIM:151510
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat how C;Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repeat C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat
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PMID:3327687
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A;Residues: 1-755,'L',757-1163 <CO3>
A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB:MB1695; EMBL:Y06093; NID:g487929; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxyl
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                              780
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NyAlternate names: leukocyte adhesion receptor p150,95 alpha chain
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: J1-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
Ciscession: A36584, A35584
J. Biol. Chem. 265, 12750-12751, 1990
A)Reference number: A36584
A)Cohents: erratum
A;Cohents: erratum
A;Accession: A36584
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                                                                                                                                   LSITPSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQNQRS
                                                                                                                                                                                                                                      841 QRSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLK
                                                                                                                                                                                                                                                               840 KKPWFVKPAESSSSSEGHGALKSTTWNINHPIFPANSEVTFNVTFDVDSHASFGNKLLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1163 <COR>
A; Molecule type: DNA
A; Residues: 1-1163 <COR>
A; Mote: this revision to the sequence from reference A35543 includes th
R; Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A; Title: Genomic structure of an integrin alpha subunit, the leukocyte
A; Reference number: A35543; MUID: 90153906; PMID:2303426
A; Rocession: A35543
A; Reference number: DNA
A; Residues: 1-834 <CO2>
A; Note: this sequence has been revised in reference A36584
R; Corbi, A.L.; Miller, LJ.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J: 6, 4023-4028, 1987
A; Title: CNA cloning and complete primary structure of the alpha subunn A; Reference number: S00864; MUID: 88166645; PMID:3327687
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A; Molecule type: DNA
A; Residues: 1-1153 <PYT>
A; Cross-references: Embl.X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Cross-references: Embl.X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Actore: the authors translated the codon CAC for residue 569 as Gln
R; Sastre L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A; Title: A partial genomic DnA clone for the alpha subunit of the mouse complement recep A; Accession: 159078
A; Reference number: 159078; WID:86287312; PMID:2942940
A; Reterence number: 159078
A; Actatus: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 11-44 REBS>
A; Rosidues: 11-44 REBS>
A; Cross-references: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
C; Genetics:
A; Conetics:
A; Cuperfamily: cell surface glycoprotein, transmembrane protein
C; Reywords: cell adhesion; glycoprotein; transmembrane protein
C; Reywords: cell adhesion; signal sequence #status preddicted cima.
F; 1-16/Domain: signal sequence #status preddicted cima.
F; 148-318/Domain: transmembrane #status preddicted cima.
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Best Local Similarity 74.5%; Pred. No. 1.7e-307;
Matches 860; Conservative 141; Mismatches 151; Indels
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EMBO J. 7, 1371-1378, 1988
A,Fitle: Amino acid sequence of the murine Mac-1 alpha chain reveals homolog A;Reference number: S00551; MUID:88312584; PMID:3044779
                                                                                SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
                                                                                                                          HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 1153; Conservative
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OM protein - protein search, using sw model

June 7, 2004, 17:05:16 ; Search time 14.7639 Seconds (without alignments) 7512.163 Million cell updates/sec Run on:

US-09-902-481B-1 5956

1 MALRVLLLTALTLCHGFNLD......FKRQYKDMMSEGGPPGAEPQ 1153 score: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR 78:* Database

pirl:* pir3:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	5956	100.0	1353	¦ -	RWHITE	Contract of the state of the st
7	4545	76.3	1153	1 (7	800551	OCVTP RUI
m	51	59.0	1163	н	RWHU1C	Surface
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S	1549	ω	1163	7	156126	nocyte fr
9	1163	19.5	1179	7	A53213	_
7	1108.5	œ	1151	N	A45226	
œ	1099	18.5	1170	N	ഹ	integrin alpha 2 g
φ.	1089	18.3	1178	N	**	otein hom
10	1087.5	18.3	1181	N	ന	-in alpha-
11	1082	18.2	1180	N	A35854	integrin alpha-1 c
12	667	11.2	1039	N	A41131	lymphocyte-Pever's
13	638	10.7	1038	N	S06046	
14	630	10.6	1035	N	I58409	
15	614.5	10.3	1041	~	T31437	alpha ch
16	579.5	7.6	1054	N	JC7294	tearin
17	572.5	9.6	1051	~	A35761	cell surface glyco
18	567.5	٠, د.	1053	N	I55534	VLA-3 alpha subuni
19	555.5	9.3	1053	N	S44250	rin alp
20	550	9.5	1034	N	A36108	integrin alpha-V c
21	535		1044	~	T10050	
22	532	•	1049	N	A27079	
23	532	•	1073	~	B36429	alr
24	530.5	8.9	1072	7	A38457	integrin alpha-6 c
25	529.5	•	1051	N	A40021	
26	O		1048	7	A27421	alpha-5
27	525.5	80	1001	~	A41543	
28	517	•	1044	Ŋ	S16516	grin alpha-8
29	505	8.5	1394	N	A29637	position-specific

integrin - fruit f	integrin alpha-2b	glycoprotein IIb -	integrin alpha-7 c	alpha-7 integrin -	leukocyte adhesion	F54F2.1 protein -	integrin alpha cha	hypothetical prote	integrin alpha v c	integrin alpha cha	integrin alpha cha	glycoprotein IIb -	integrin alpha cha	integrin alpha-1 -	glycoprotein IIb -
840311	A34269	A60163	JC5950	161186	B30892	S44824	\$38783	S28277	S60571	T09433	T09403	136916	T18523	A55348	136917
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1146	1039	1037	1137	1135	126	1226	1106	1139	1045	1115	1115	764	1086	272	604
8.3	۳. ش	8.3	8.2	8.2	8.2	9.0	7.9	7.6	7.6	7.2	7.1	9,9	5.2	S.	5.0
496.5	495.5	492.5	490	488	486	474.5	469.5	454.5	454	430.5	423.5	391	309	304.5	299
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ALIGNMENTS

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MyAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein NyAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Neukocyte integrin alpha chain, neutrophil adherence receptor alphaM chain C;Species: Homo sapiens (can)
C;Bate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2000
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #a2218; A46526; A26091; I52567
B;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, C

A; Reference number: A31108; MUID:88315033; PMID:2457584

Ajacession: A31108
A;Molecule type: mRNA
A;Residues: 1-1153 <CORA;Residues: 1-1153 <CORA;Residues: 1-1163 <CORA;Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence of the alpha subunit of human leukocyte adhesion receptor
A;Reference number: A28915; MUID:88257215; PMID:2454931
A;Molecule type: mRNA

A; Molecule type: mRNA
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Ross-references: GB:MIGN44, GB:M103-070, GB:M19664, GB:X07421; NID:g186935; PIDN:AAA56
A; Note: part of this sequence, including the amino end of the mature protein, was confi
R; Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally re
A; Reference number: A41600, MUD:92073318; PMID:1683702
A; Rosidues: 1-9 <ARN>
A; Residues: 1-9 <ARN>
A; Residues: 1-9 <ARN>
A; Residues: 1-9 <ARN>
A; Remod-O'Donnell, B.; Pierce, M.W.; Harris, P.; Tenen, D.G.
B; Arnaout, M.A.; Remod-O'Donnell, B.; Pierce, M.W.; Harris, P.; Tenen, D.G.
A; Reference number: A81,93; MUD:88190151; PMID:2833753
A; Rocession: A30892.
A; Rocession: A30892.

A; Molecule type: mRNA A; Residues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> A; Tesidues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> B; Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. R; Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. A; Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor A; Reference number: A3218; MUID:8908893; PMID:2563162 A; Accession: A3218 A; Accession: A3218 A; Accession: A3218 A; Accession: A3218 A; Coss-references: GB:J04145; NID:g189068; PIDN:AAAS9903.1; PID:g386975

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                                                                                                                                                                                                                                           Length 1161;
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| APPLICANT: Van der Vieren, Monica | 11TIL2 OF INVENTION: No. US20030077278Alel Human 2 | FILE REFERENCE: 27866/35004 | CURRENT APPLICATION NUMBER: US/09/891,943 | CURRENT FILING DATE: 2001-06-26 | RRIOR APPLICATION NUMBER: US/193,043 | PRIOR PILLING DATE: 1998-11-16 | PRIOR APPLICATION NUMBER: 09/193,043 | PRIOR FILLING DATE: 1994-06-05 | PRIOR FILLING DATE: 1994-02-05 | PRIOR FILLING DATE: 1994-12-21 | PRIOR APPLICATION NUMBER: 08/362,652 | PRIOR APPLICATION NUMBER: 08/363 | PRIOR APPLICATION NUMBER: 08/363 | PRIOR FILLING DATE: 1997-10-03 | PRIOR FILLING DATE: 1997-10-03 | PRIOR FILLING DATE: 1997-10-03 | SEQ ID NOS: 114
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                    LENGTH: 1161
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US-09-891-943-2
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780
                   912 QLELPVKYAVYTMISRQESTKYFNPATSDEKAMKEABHRYRVANLSQRDLAISINFWVP 971
                                                                                       794 SSLELNVIVTVWNAGEDSYGTVVSLYYPAGLSHRRVSGAQKQPHQSALRLACETV-PTED
SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNI CQDDLSTTFSFMSLDCLVVG
                                                                    GPREFNVTVTVRNDGEDSYRTOVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                                                                                                                                                                                                             QLELPVKYAVYMVTSHGVSTXYLNF-TASENTSRVMQHQYQVSNLGQRSLPISLVFLVP
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earch completed: June 7, 2004, 17:38:44 ob time : 42.8905 secs

360 375 420 435 480 495 540 555 600 615 660 673 720 733 780 793 840

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960 VRINQTVIWDRPQVIPSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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                             RIHFTFKEFONNPNPRSLIKPITOLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
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US-09-891-943-2
IS-09-891-943-2
; Sequence 2, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
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                                                                      GPREFNUTVIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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larity 58.9%; Pred. No. 5e-304;
Conservative 168; Mismatches 288; Indels 8
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Aiel Hum
FILLE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT APPLICATION NUMBER: 03/13,497
EARLIER APPLICATION NUMBER: 03/13,497
EARLIER APPLICATION NUMBER: 03/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-10-05
EARLIER PILING DATE: 1994-10-03
NUMBER: OF SEO, DI NOS: 114-06
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; Sequence 2, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    (FOTENTIAL)
(POTENTIAL)
SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 1 VWPA domain. SIMILARITY: Contains 7 FG-GAP repeats.
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MEDLINE-94193647; PubMed=7511592;

MEDLINE-94193647; PubMed=7511592;

T Identification of putative ligand binding sites within I domain of integrin alpha 2 beta 1 (VIA-2, CD49b/CD29).";

T integrin alpha 2 beta 1 (VIA-2, CD49b/CD29).";

C J = 101. Chem. 269:9659-9663(1994).

C OLLAGEN, COLLAGEN C-PROPERTIDES, FIBROMECTIN AND B-CADHERIN.

C COLLAGEN, COLLAGEN C-PROPERTIDES, PIBROMECTIN AND B-CADHERIN.

C COLLAGEN IT IS RESPONSIBLE FOR ALHESION OF PLATELETS AND OTHER COLLAGEN. TO IS RESPONSIBLE FOR ALHESION OF PLATELETS AND OTHER EXPRESSION, FORCE GENERATION AND ORGANIZATION OF NEWLY SYNTHESIZED EXTRACELLULAR MATRIX.

C --- SUBUNIT: HETRERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-2
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                                                                                                                                                                                                                                    ERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWY---- 1057
                                                                                                                                                                                                                                                                                     IKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPN-----PLPLIV 1111
                                     836
                                                                                    896
                                                                                                                                    949
                                                                                                   872 KEDSDGS--IRCVNEER-----RLOKQVCNVSYPPFRAKAKVAPRLDPEF-SKSIFLHHL 923
                                                                                                                                                           924 EIELAAGSDSNERDSTKEDNVAPLRFHLKYEADVLFTRSSSLSHYEVKLNSSLERYDGIG 983
                                                           871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein, DOMAIN: THE INTECRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
: | : | : | ----DHGRPTTLRYSVPFWNGCNEDEHCVPDLVLDARSDLPTAMEYCQRVLRKP
                                                    AQDCSAYTLSFDTTVFIIESTRQRVAVEATLENRGENAYSTVLNISQSANLQF--ASLIQ
                                                                                    NORSORSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITPDVDSKASLGNKL
                                                                                                                                    LLKANVTSENNMPRINKTE--PQLELPVKYAVYMVTSHGVSTKY---LNFTAS--ENTS
                                   ----SITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
28-F82-2003 (Rel. 41, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa)
(Collagen receptor) (VLA-2 alpha chain) (CD49b) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "III TUDGETINS TO NOT UNDERSOY EXCERNING CHARLES."
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                     GSSVGGLLILALITAALYKLGFFK--RQYKDMMSEGGPPGAEP 1152
                                                                                                                                                                                                                                                                                                                                                 PRT; 1170 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATES WITH BETA-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVM
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CELL ATTACHMENT SITE (POTENTIAL)
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5e-65;
as its content
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                            PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                   Polymorphism; Calcium;
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27.8%; Pred. No. 5e-6!
tive 215; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              FG-GAP 1.
FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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N-LINKED
                                                                   EMBL; L25886; AAB59255.1; -.
PIR; 145914; 145914.
HSSP; P17301; 1AOX.
InterPro; IPRO00413; Integrin_alpha.
InterPro; IPRO00315; VWF A.
Pfam; PPO01839; PG-GAP; 3.
Pfam; PPO01837; integrin_A; 1.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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1010 DFLAE-LRKAPUVNCSIAVCQRIQCDIPFFGIQEBFNATLKGNLSFDWYIKTSFNHLLIV 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 SMA-----SVIIHIPQYIKOKNPLMYLTGVHTDQAGDISCEABINPLKIGQTSSSV 1024
YTTGVCSDVSPDF-QERTSPAPAVQTCP-SFIDVVVVCDESNSIYPWD--AVRNFLEKFV 189
                                                                                       287
                                                                                                                                                                                                                                                                                                      231
                                                                                                       CYARDTAYSTAAGGRPGATKVWVVTDGESH-DGSKLKAVIDQCNKDNILRFGIAVLGYL 304
                                                                                                                                                            NRNALDTKNLIKEIKAIASIPTERHFFNVSDEADLLEKAGTIGEQIFSIEGTVQG-GDNF 363
                                                                                                                                                                                                    CMEMSQVGFSAEYSPQNNILMLGAVGAYDMSGTVVQXTPHGHLIPSKQAFEQILQDRNHS 423
                                                                                                                                                                                                                                      AYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRONTGMESNANV-----KGTQIGA 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAFGNLRPVLAEDAQRLFTALFPFERNCGNDNICQDDLSITF----SFMSLDCLVVGGPR 799
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                                                        QGLDIGPTKTQMGLIQYANNPRVVFNLNTFKSKD----EMIKATSQTFQYGGDLTNTFKAI
                                                                                    RKVVRELFNITNGARKNAPKILVVITDGEKFGDPLGYBDVIPEADREGVIRYVIGV----
                                                                                                                                                                                                                                                       SQKSVICNVGYPALKSKQQVTFTINFDFMLQ-NLQNQASISFRALSBSQEENMADNSVNL
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                                                                                                                                      -GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSF
                                                                                                                                                                                                                                                                                         YPGASLCSVDVDSNGSTDLVLIGAPHYYBQTR--GGQVSVCPLPRGQRARWQCDAVLYGB
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TOOMDIGE DATECTION OF EXPRESSION SUGGEST EXTENSIVE TO BE TO THE AIDHA STATEMENTS OF EXPLESSION IN MUNICE GEVELORMENT.";

Dev. Dyn. 199:292-314(1994).

CC -1- FUNCTION: INTEGRIN ALPHA-1 IS A COLLAGEN RECEPTOR, BEING RESPONSIBLE FOR ADHESTON OF PLATELETS AND OTHER CELLS TO COLLAGENS, MODULATION OF COLLAGEN AND COLLAGENSE GENE EXPRESSION, FORE GENERATION AND ORGANIZATION OF NEWLY SYNTHESIZED EXTRACELLULAR MATRIX. IT IS ALSO A RECEPTOR FOR LAMININS, COLLAGEN C-PROPERTIDES AND E-CADHERIN. INCE HOWOXYGOUG FOR A NULL MUTATION IN THE ALPHA-2 DIE VERY REALY IN EMBRYOCENSIS.

C-PROPERTIES AND E-CADHERIN. IN EMBRYOCENSIS.

C-SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-2 ASSOCIATES WITH BETA-1.

C-1- SUBUNIT: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

C-1- SUBLIARITY: CONLAINS 10 WFA GOMAIN.

C-1- SIMILARITY: CONLAINS 10 WFA GOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        Edelman J.M., Chan B.M., Uniyal S., Onodera H., Wang D.Z., Damjanovich L., Latzer D.B., Finberg R.W., Bergelson J.M.; "The mouse VLA-2 homologue supports collagen and laminin adhesion but not virus binding."; Cell Adhes. Commun. 2:131-143(1994).
                                                                                                                                                                                            glycoprotein Ia) (GPIa)
                                                                                                                                                                                                                                                                     Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                            Q62469; Q62163;
15-JUL-1998 [Rel. 36, Created)
15-JUL-1998 [Rel. 36, Last sequence update)
28-FEB-2003 [Rel. 41, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane g
(Collagen receptor) (ViA-2 alpha chain) (CD49b)
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HSSP: P17301; LACX.
MGD; MGI:9660; LGG2.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
1135 LLALVAILWKLGFFKRKYEKM 1155
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Lung;
MEDLINE-9435561; PubMed=7521231;
Wu J.E., Santoro S.A.;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6 X CBA; TISSUE=Lung
MEDLINE=94363406; PubMed=8081889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE OF 450-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PP001839; FG-GAP; 3.
Pfam; PP001837; integrin_A; 1.
Pfam; PP00092; vwa; 1.
SMART; SM00191; Int alpha; 4.
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                                                                                              STANDARD;
                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                              MOUSE
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973 KVTAGŠAPVSMALVTIHIPQYTKEKNPLLYLTGIQTDQAGDISCTABINPLKLPHTA--- 1029
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    859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 IVSNQNKRLTFSVILKNRGESAXMTVVLAEFSENLFP------ASFSMPVDGTE
                                                                                                                                                                                                                                                                                LVVGGPREFNVTVTVRNDGBDSYRTQVTFPPPLDLSYRKVSTLQNQRSQRSWRLACESAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            860 VICEVGSSQKSVICDVGYPALKSBQQVIPTINFDFNLQ-NLQNQAAINPQAFSESQ--ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912 NKTE--FØLELPVKYAVYMVVTSHGVSTKYLNPTASENTSRVMQHQYQVSNLGQR----
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                                                                                               ORIAGSKLSPR--LOYPGOSLSGGODLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMBF
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                                                                                                                                                                                          684 GRPHSRAVFNETKNSTRRQTQVLGLTQTCET--LKLQLPNCIEDPVSFIVLRLNPSLVGT
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TISSUE-Endothelial cells;
MEDLINE-89308879, PubMed=2545729;
Takada Y., Hemler M.E.;
Tikada Y., Hemler M.E.;
The primary structure of the VLA-2/collagen receptor alpha 2 subunit (platelet GPIa): homology to other integrins and the presence of a
                                                                       LYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHS
                                                                                                                                                                                                                                                     628 NPREVARNVPECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----S
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxiD=9606;
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia)
(Collagen receptor) (VLA-2 alpha chain) (CD49b).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-GDNFQMEMAQVGFSADYAPQNDIIMIGAVGAFDWSGTLVQETSHKPVIFPKQAFDQVL 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 QDRNHSSFLGYSVAAISTEDGVHFVAGAPRANYTGQIVLYSVNK---QGNVTVIQSHRGD
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CELL ATTACHMENT SITE (POTENTIAL)
GPFKR MOTIF.
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                                          INTEGRIN ALPHA-2.
EXTRACELLULAR (POTENTIAL).
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CTOPLASMIC (POTENTIAL).
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FG-GAP 4.
FG-GAP 5.
FG-GAP 5.
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Pfam; PF01839; FG-GAP; 3.
Pfam; PF001839; FG-GAP; 3.
Pfam; PF001957; integrin_A; 1.
Pfam; PF000927; vwa; 1.
SWART; SM00191; Int alpha; 5.
SWART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS0234; VWPA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Platelet; Signal; Repeat; Calcium; Magnesium; Polymorphism;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
INTERACTION WITH HPSS.
       GO, GO:0007160; P:cell-matrix adnesion; 145.
GO; GO:0007397; P:histogenesis and organogenesis; TAS.
InterPro; IPR001913; Integrin_alpha.
InterPro; IPR020395; WF.A.
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FG-GAP 3.

FG-GAP 4.

FG-GAP 6.

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FG-GAP 7.

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dbSNP:1801106).
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         THEOMO. Haemost. 83:392-396(2000).

THICOMO. Haemost. 83:392-396(2000).

THICOMO. HAEMOST. 83:392-396(2000).

COLLAGEN, COLLAGEN C. PROPERTIOSS, FIRSONECTIN AND E-CADERAIN. IT RECCONIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-B-R IN COLLAGENS. IT IS RESPONSIBLE FOR ADHESTON OF PLATELETS AND OTHER CELLS TO COLLAGENS. IT IS RESPONSIBLE FOR ADHESTON OF PLATELETS AND OTHER CELLS TO COLLAGENS. IT IS RESPONSIBLE FOR ADHESTON OF PLATELETS AND OTHER SEXPRACESLULAR MATRIX.

SUPPLISATION AND ORGANIZATION OF NEMLY SYNTHESIZED SEXPRACESLULAR MATRIX. The mambrane protein.

SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-2 associates with beta-1. Interacts with HPS5.

SUBURIT: HETEROTIVE TYPE I MEMBRANG PROFESAS CLEAVAGE.

SUBURITY: BOORTION 534 is associated with platelet-specific alloanting here. FollyMorphism position 534 is associated with platelet-specific alloanting here. FollyMorphism position 534 is associated with platelet-specific alloanting here. HPA-56 (BR). HPA-57 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20206009; PubMed=10744142; Kroll H., Gardemann A., Fechter A., Haberbosch W., Santoso S.; "The impact of the glycoprotein Ia collagen receptor subunit A1648G gene polymorphism on coronary artery disease and acute myocardial
                                                                                                                                                                                                                                                                                                                                     "The human platelet alloantigens Br(a) and Brb are associated with sale amino acid polymorphism on glycoprotein Ia (integrin subunit
                                                     SEQUENCE FROM N.A. Riddanek S.A., Riddanek S.A., Riddanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 168-368.
MEDLINE=9801923; PubMed=3353312;
Ensley J., King S.L., Bergelson J.M., Liddington R.C.;
"Crystal structure of the I domain from integrin alpha2betal.";
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Santoso S., Kalb R., Walka M., Kiefel V., Mueller-Eckhardt C.,
Newman P.J.;
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EMBL; AF512556; AAM34795.1; -.
PTR, A33989; A33998.
PDB; 1DZ1; 02-AUG-01.
Genew; FACK: 6137; ITGA2.
MJM; 192974; -.
GO; GO:0005886; C:integrin complex; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005886; F:coll adhesion receptor activity; TAS.
GO; GO:0005895; F:collagen binding; TAS.
GO; GO:0005896; P:blood coagulation; TAS.
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possible collagen-binding domain.";
J. Cell Biol. 109:397-407(1989).
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Homo sapiens (Human)
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Best Local Similarity 27.3%; Pred. No. 3e-64;
Matches 339; Conservative 214; Mismatches 498; Indels 193;
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987 PQVTF-SENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFN 1045
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SST-EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPR 910
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Widely expressed with highest expression in muscle and heart. Found in articular cartilage.
DOWAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 VWFA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
                                                     862 EVICQVAASQKSVACDVGYPALKREQOVIFIINPDFNLO-NLONQASLSFQALSESQEEN
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"Isolation, cloning, and sequence analysis of the integrin subun
alphal0, a betal-associated collagen binding integrin expressed
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TISSUBE-Bndothelial cells, and Heart;
MEDLINE-20169197; Pubmed-10702680;
Lehnert K., Ni J., Leung E., Gough S.M., Morris C.M., Liu D.,
Wang S.-X., Langley R., Krissansen G.W.;
"The integrin alphalo subunit: expression pattern, partial gene
structure, and chromosomal localization.";
Cytogenet. Cell Genet. 87:238-244(1999):
-!- FUNCTION: INTEGRIN ALPHA-10/BETR-11 S. RECEPTOR FOR COLLAGE
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo
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J. Biol. Chem. 273:20383-20389(1998)
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TISSUE=Articular chondrocytes;
MEDLINE=98352078; PubMed=9685391;
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LSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTETKVBPFBVPPLPLIV 1111
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RRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHP...----AVNMHLGMSLLETDGDGG
                                                                    IPHD----FRRM--KEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSL
                                                                                                                                                                                                                                                    273 PEADREGVIRYVIGY-GDAFRSEKS----ROBLNTIASKPPRDHVFOVNNFEALKTIONO
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Best Local Similarity 29.6%; Pred. No. 3.9e-64;
Matches 366; Conservative 196; Mismatches 492; Indels 183; Gaps
                                                                                                                                                                                                                                                                                   DR InterPro; IPROCO413: Integrin_alpha.

BR InterPro; IPROCO413: Integrin_alpha.

BR PÉAN; PFO0092; VWP, A.

BR PRINTS; PRO1185; INTEGRINA.

BR PRINTS; PRO1185; INTEGRINA.

BR PRINTS; PRO0491; INTEGRINA.

BR PRINTS; PRO0491; INTEGRINA.

BR PRAFT; SW00191; INT_alpha; 4.

BR PROSITE; PSOCO442; INTEGRINA ALPHA; PALSE_NEG.

BR PROSITE; PSOCO342; UNFA; I.

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G -> V (IN REF. 2).
E -> D (IN REF. 2).
MW; AE7D3A1C25C1AEA0 CRC64).
                                                                                                                                                                                                                           GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0004895; F:cell adhesion receptor activity; TAS.
GO; GO:0005518; F:cellagen binding; TAS.
GO; GO:0007160; P:cell-matrix adhesion; TAS.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
FG-GAP 2.
VWFA.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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EMBL, AF112345; AAF21944.1; -.
EMBL, AF172723; AAF61638.1; -.
HSSP, P17301; 1AOX.
Genew; HGNC:6135; ITGA10.
MIM; 604042; -.
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                                                                                                                                                                                                                                                                                                                                 E-R IN COLLAGEN.

-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
ASSOCIATES WITH BETA-1.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- DOMAIN: THE INTEGRIN I-DOMAIN (INSER!) IS A WWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

-1- SIMILARITY: Belongs to the integrin alpha chain family.

-1- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R PDB; ICK4; 03-MAY-00.

R InterPro; IPR00013; Integrin_alpha.

R InterPro; IPR00135; VWF_A.

Friam; PF001839; FG-GAP; 3.

R Pfam; PF001837; integrin_A; 1.

R SMART; SM00191; Int alpha; 5.

R SMART; SM00192; VWF_A. 1.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.

R PROSITE; PS00244; VWFA, 1.

R PROSITE; PS00244; VWFA, 1.

R SMART; SM0181; INTEGRIN_ALPHA; 1.

R PROSITE; PS00244; VWFA, 1.

R SMART; SM0181; PS0184; VWFA, 1.

R Integrin; Call adheaton; Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Callium; Magnesium; 3D-structure.

I SIGNAL

I CHAIN

29 1180 INTEGRIN ALPHA-1.

I CHAIN

29 1142 EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                            Ignatius M.J., Large T.H., Houde M., Tawil J.W., Barton A., Esch F., Carbonetto S., Reichardt L.F.; Molecular cloning of the rat integrin alpha 1-subunit: a receptor for laminin and collagen.";

J. Cell Biol. 111:709-720(1990).
                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11negrin alpha-1 precursor (Laminin and collagen receptor) (VLA-1)
(CD49a).
            1112 GSSVGGLLLLALITAALYKLGFF-----KRQYK 1139
                         1128 GSVLGGILLLALLVFCLWKLGFFAHKKIPEEEKREEK 1164
                                                                                                                                                                                                                                [1] __
SEQUENCE FROM N.A.
MEDLINE-90338125; PubMed=2380249;
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                                                                                          STANDARD;
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Rattus norvegicus (Rat)
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18.2%; Score 1082; DB 1; Length 1180;
Best Local Similarity 27.7%; Pred. No. 6.9e-64;
Matches 351; Conservative 199; Mismatches 484; Indels 234;
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Description	Q9ji30 rattus norv Q8ca73 mus musculu	Q28984 sus scrota Q81va6 homo sapien O90xh4 mus musculu	090ye7 rattus norv 090yt4 mus musculu	Q9r200 mus musculu Q98tfl cyprinus ca	Q96hbl homo sapien Q86hbl homo sapien Q8hzv0 bos taurus	088340 rattus norv 088341 rattus norv 042094 gallus gall	Oleda musculu
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ALIGNMENTS

	PRT; 1151 AA.	Created)	Last sequence update) Last annotation undate)			Craniata; Vertebrata; Buteleostomi; Sciuroquathi; Muridae; Murinae; Rattus.				CD11b cDNA sequence.";	:/GenBank/DDBJ databases.			lex; IEA.	Ficell adhesion receptor activity; IEA.	Thesion; IEA.	lpha.								1; T:	8F785695D4074CA5 CRC64;	Score 4459; DB 11; Length 1151;	; Fred. No. 2.38-315; 144; Mismatches 160; Indels 2; Gaps
RESULT 1 29JI30	Q9JI30 PRELIMINARY;	-	01-UCI-2000 (TERMBLEEL. 15, 01-JUN-2003 (TERMBLEEL. 24.		Rattus norvegicus (Rat)	Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;	NCBI_TaxID=10116;	SEQUENCE PROM N.A.		"Cloning of the rat CD11b	Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases	EMBL, AF268593, AAF81280.1;	HSSP; P11215; 1BHO.	GO; GO:0008305; C:integrin complex; IEA.	GO; GO: 0004895; F:cell ad	GO; GO: 0007160; P:cell-matrix adhesion; IEA.	InterPro; IPR000413; Integrin_alpha.	INTERFECT LFROUZUSS; VMF.		00092; vwa; 1.	PRINTS; PR01185; INTEGRINA.	PRINTS; PRO0453; VWFADOMAIN	SMART; SM00191; Int_alpha;	SMART; SM00327; VMA; 1.		1151 AA; 126	Query Match 74.9%;	vat
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01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
11-CCT-2003 (TYEMBLREL. 23, CANOTATE)
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POKPPEALRGCPQQESDIAFLIDGSGSINRLDPQRMKEFVSTVMGQPQKSKTLFALMQYS
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                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
64.2%; Score 3824.5; DB 6; Length
Best Local Similarity 79.8%; Pred. No. 3.2e-269;
Matches 735; Conservative 77; Mismatches 108; Indels
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus
NCBI_TaxID=9823;
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920 AA; 102440 MW; B96CC51B350DD5AC CRC64;
                                                  SEQUENCE FROM N.A.

Lee J.-K., Schook L.B., Rutherford M.S.;
Loss J. 440072; AAB166891; --
HSSP; P11215; 1BHQ.
Colon08305; C:integrin complex; IEA.
GG; GG:00008305; C:integrin complex; IEA.
GG; GG:0000413; Integrin alpha.
InterPro; IPR000413; Integrin alpha.
InterPro; IPR000413; Integrin alpha.
FEAN; PF00189; VWF, A.
FEAN; PF00189; VWF, A.
FEAN; PR00189; INTEGRINA.
FRINTS; PR00453; VWFADOWAIN.
SWART; SWO037; VWF, 1.
FRINTS; PR00191; VWFA; 1.
FROM; TER.
SWART; SWO037; VWFA; 1.
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SWART; SWART; SWO037; VWFA; 1.
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SWART; SWART; SWO037; VWFA; 1.
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SWART; SWART; SWART; VWFA; 1.
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                      NTIASKPRDHVRQVNNFBALKTIQNQLREKI FAIBGTQTGSSSSFEHEMSOBGFSAAIT 360
                                                                                             SNGPLLGSVGSFDWAGGAFLYTSXDKVTFINTTRVDSDWDAYLGYASAVILRNRVQSLV 420
                                                                                                                                                                                                   HYYEQTRGGQVSVCP1PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA 540
                                                                                                                                                                                                                                                          541 IGAPGEEDNRGAVYLFHGISGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
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                                                                                                                                                                                                                                                                                                                      601 DLTVGAQGHVLLLRSQPVLRVKAIMEPNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK 660
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                                                                                                                                                          LSITFSFMSLDCLVVGGPREFNYTVTVRNDGEDSYRTQVT?FFFPLDLSYRKVSTLQNQRS
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Q28984; PRELIMINARY; PRT; 920 AA.
Q18984; Q1-NOV-1956 (TrEMBLrel. 01, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-FEB-1997 (TrEMBLrel. 24, Last annotation update)
C011b (Fragment).
CD11b (Fragment).
CD11b (Fragment).
Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                246 ARRDAAKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKELNDIA 305
                                                364
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                                                                                                           366 VLGAVGSFTWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQSLVLGAP 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                785 PSPPGLKSLLVGSNLELNAEVMVWNDGEDSYGTTVTPSHPAGLSYRYVAEGOKOGOLKSL
   ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQBLNTIA
                                                SKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP
                                                             306 SKPSQEHIFKVEDFDALKDIQNQLKEKIFALEGTETTSSSSFELEMAQBGFSAVFTPDGP
                                                                                                                                                       QTRGGQVSVCPLPRGWR-RWWCDAVLYGBQGHPWGRFGAALTVLGDVNGDKLTDVVIGAP
                                                                                                                                                                                                                                   GEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTV
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                                                                                             LLSTVGSYDWAGGVFLYTSKBKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
                                                                                                                                        RYQHIGLVAMPRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
                                                                                                                                                                                       QTRGGQVSVCPLPRGQRARWQCDAVLYGBQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP
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090XH4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Leukocyte adhesion glycoprotein p150,95 alpha integrin subunit.
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                                                                                TEPOLELPVKYAVYMVVTSHGVSTKYLNPTASENTSRVMOHOYOVSNLGORSLPISLVFL 973
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                                                TEESTALKSISCSINHPIFPDNSEVTFNVTFDVNPDAFLGYKLLKANVTSENNMPSSNK
                                                                                                                            TEFQLELPVKYAVYVVVTSLEVSTKYFNFTASEKTRHVIEHQYQFNNLGQRKLPISVVFW
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                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Integrin, alpha X (Antigen CDIIC (pl50), alpha polypeptide).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 61.5%; Pred. No. 1.9e-246;
hes 702; Conservative 138; Mismatches 295;
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                                                                                                                                                                                                                                                           1169
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                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                           DIPFFGIQEEFNATLKGNLSF 1054
                                                                                                                                                                                          DIPSFGIQEELKVTLKGNLSF 920
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01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                           PRELIMINARY;
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                ۵,
  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                       1169 AA; 129150 MW; C616412033C219A6 CRC64;
                                                                                            PROSITE; PS00242; INTEGRIN ALPHA, 1.
PROSITE; PS50234; VWFA, 1.
             NCBI_TaxID=10090;
                                                                                                   Integrin.
SEQUENCE
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Gaps Query Match 56.3%; Score 3352.5; DB 11; Length 1169; Best Local Similarity 57.1%; Pred. No. 1.1e-234; Matches 657; Conservative 168; Mismatches 307; Indels 19;

125 128 126 FGSNIRQQPQKPPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQLKKSKT 185 187 245 247 305 307 KPPRDHVPQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPL 365 65 68 66 CDYSTGSCEPIRLQVPVEAVMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFL CGYHTGNCEPISLQVPPEAVNISLGLSLAAATNPSMLLACGPTVHHTCRENIYLTGLCFL 188 RFSLMQPSDXFRVHFTFNNFISTSSPLSLLGSVRQLRGYTYTASAIKHVITELFTTQSGA 248 RQDATKVLIVITDGRKQGDNLSYDSVIPMABAASIIRYAIGVGKAFYNEHSKQELKAIAS RKNAPKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQBLNTIAS LLLTALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQBIVAANQRGSLYQ LFSLMQYSBEPRIHFTPKEPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRBLFNITNGA σ 69 186 306 ò 쉱 ⋩ 움 & 셤 ઠે Db <u>පි</u> ර 8 g

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REDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVG 605

546

1073 725 724 785 784 836 844 894 902 HOYOVSNLGORSLPISLVFLVPVRLNOTVIWDRPQVTFSSNLSSTCHTKERLPSHSDFLA ::| | | | | | | | | ::| : | | | | ::| : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | : | | | : | | : | | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 837 --NQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGN 1014 ELRKAPVVNCSIAVCORIOCDIPFFGIQEFFNATLKGNLSFDWYIKTSHNHLLIVSTABI 606 AQGHVLLLRSQPYLRVKAIMBFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDR 726 PVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITF 786 SEMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFPPPLDLSYRKVSTLQ-----FKROYKOMMSE 1144 954 1134 के है के 셤 숨 ਨੇ

Alpha D integrin.
Rattus norvegicus (Rat).
Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116; Created)
Last sequence update)
Last annotation update) PRT; 1161 AA. 090YE7; 01-MAY-2000 (TIEMBLEEL: 13, 01-MAY-2000 (TIEMBLEEL: 14, 01-JUN-2003 (TIEMBLEEL: 24, PRELIMINARY; **090YE7**

STRAIN-Sprague-Dawley;

C STRAIN-Sprague-Dawley;

C O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,

Gallatin W.M.;

"Cloning of rat alpha D, a novel beta 2 integrin.";

Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

E MEDL; AF021334; AAF2124.1.; -.

R HSSP; P11215; 18HQ.

R GO; GO:0008305; C:integrin complex; IEA.

R GO; GO:000495; F:cell adhesion receptor activity; IEA.

R GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.

R GO; GO:0007239; Wefa.

R InterPro; IPR00413; Integrin_alpha.

InterPro; IPR00413; Integrin_alpha.

R Ffam; PF01839; FG-68AB; 3.

R Ffam; PF00357; integrin_A; 1. RESULT 6

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TSENNMPRINKTEFOLEL PVKYAVYMVVTSHGVSTKYLNFTASENTSR-VMOHQYQVSNL
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ilarity 34.0%; Pred. No. 4.6e-103;
Conservative 219; Mismatches 462; Indels 108;
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Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                         PRELIMENARY;
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Best Local Similarity
Matches 407, Conserva
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ML 1136
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                                                                                                                                          6 VILLCGWVLASCHGSNLDVBEPIVFREDAASFGQTVVQFGGSRLVVGAPLEAVAVNQTGR
                                                                                                                                                                              66 LYDCAPATGMCQPIVLRSPLEAVNMSLGLSLVTATNNAQLLACGPTAQRACVKNMYAKGS
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                                                                                                                               5 VILLIT -- ALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQBIVAANQRGS
                                                                                                             Gaps
                                                                                         Ouery Match 55.1%; Score 3282.5; DB 11; Length 1161; Best Local Similarity 58.1%; Pred. No. 1.4e-229; Matches 663; Conservative 158; Mismatches 306; Indels 15;
                                                                       1161 AA; 126600 MW; 2258491A984A705E CRC64;
Prints, Pro192; vwa; 1.
PRINTS; PRO1945; VWEADOWAIN.
SWART; SM00191; Int_alpha; 4.
SWART; SM00237; vwa; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
                                                                 Integrin.
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1081 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQYKD 1140
1075 SQLPGQEAFLRAQVETTLESYVVYEPIFLVAGSSVGGLLLIALITVVLYKLGFFKRQYKB 1134
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus. TaxID=10090;
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Ma R.Z., Teuscher C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APO659JG, AAD25884.1; -.
HSSP; P20701; 1LFA.
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GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0004895; F:cell adhesion receptor act
GO; GO:0007160; P:cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
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PRINTS; PRO185; INTEGRINA.
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SWART; SMO0191; Int_alpha; 5.
SWART; SMO037; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                 SGEDAYWVRLDLDFPRGLSFRKVEMLQ---PHSRMPVSCBEL--TEGSSLLTKTLKCNVS 859
                                                                                                                                                                                                                                                                                                                                                                                              HPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSEN-NMPRINKTEFQLELPVKYAVY 927
                                              IRWFGRSIHGVKDLGGDRLANVVVGPEGRVVVLSSRPVVDVVTELSFSPEEIPVHEVECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGAAL TVIGDVNGDKG.TDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR
                                                                                       LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMBFNPREVARNVFECN
                                                                                                                                                   641 DQVVKGKEAG-EVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNST
                                                                                                                                                                      RROTOVLGLTQTCETLKLQLPNCIEDPVSPIVLRLAPSLV---GTPLSAFGN-LRPVLAE
                                                                                                                                                                                                                                                                       DAQRLFTALFPFEKNCGNDNI CQDDLSI TFSFMSLDCLVVGGP-----REFNVTVTVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRP
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LCSVDLDQDGBABILLLIGAPLFFGEQRGGRVFTY---QRRQSLFEMVSELQGDFGYPLGR
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Bukaryota, Metazoa, Chordaca, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes, Cyprindae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DITHEKEMEHVYVESGIGGLVELFELFLALAYKVGFFKRALKEKMEADGGVPNGSP
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GO:0004190; F:aspartic-type endopeptidase activity; IRA.
GO:0004895; F:cell adhesion receptor activity; IRA.
GO:0007160; F:cell-matrix adhesion; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Peritoneal exudate cells;
Kimura M., Makao M., Mura C., Fujiki K., Yano T.;
"Molecular Cloning of a leukocyte integrin from the communited (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB04835; BA393134.1; -.
HSSP; P20701; LLFA.
CO, GO:0008305; Cintegrin complex; IRA.
CO, GO:0004180; F:aspartic-type endopectidase activity;
CO, GO:0004895; F:cell adhesion receptor activity;
CO, GO:0004895; F:cell adhesion receptor activity;
CO, GO:0004895; F:cell-matrix adhesion; IRA.
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01-JUN -2001 (TEMBLES]. 17,
01-OCT -2003 (TEMBLES]. 25,
CD11-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 STGEMYSCTADLQSCQ--RLQRPGSESVRFFGMSAAVSSAALTS-----CSPYFPHECD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 QSGFSVVYQEESVIVGSVGSNDWRGALYEVTG-SGSDFKETEIIDPAVNKDSYMGYSTVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 LKNLLNSMLSGADSKAQKALVIITD----GDPSDNDYNVLKKCDEQNILRYIIGVG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 QEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMN-DAYLGYAAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 STDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQ-----GQPWGRFGAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 ILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                144;
                                                                                                                                                                                                                                                                                                                                                                                Length 1196;
                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.8%; Score 1419; DB 13; Length Best Local Similarity 31.3%; Pred. No. 7.3e-94; Matches 377; Conservative 228; Mismatches 455; Indels
                                                                                                                                                                                                                                                                                                                              1196 AA; 132477 MW; 9369C807E7DCA53B CRC64;
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001969; Asprotease AS.
R InterPro; IPR000413; Integrin_alpha.
R Ffam; PP01839; PG-GAP; 3.
R Pfam; PP01839; PG-GAP; 3.
R Pfam; PP01839; PG-GAP; 3.
R Pfam; PP00185; INTEGRINA.
R PRINTS; PR01185; INTEGRINA.
R PRINTS; PR01185; INTEGRINA.
R PRNST; SM00137; VWA; 1.
R PR051TE; PS00141; ASP PROTEASE; 1.
R PROSITE; PS00141; ASP PROTEASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 ÓSGFSVVYQEESVIVGSVGSNDWRGALYEVMGSGSKFRQTRÍTDPAVN---KDSYMGYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| :| :| | | :| : | | | : : | | : DGDSDFLLVGAPLFYQSQPRAEGRLYVYTL-----SEQYSQKTLQSTTGRFATS
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                                                                      LRVLLLTALTLCHGFNLDTENAMTFQENARG-FGQSVVQLQ-GSR--VVVGAPQEIVAAN
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         Pred. No. 3.4e-90;
; Mismatches 460;
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         ilarity 31.4%; Pro
Conservative 210;
      Best Local Similarity
Matches 379; Conserv
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TISSUE=Peritoneal exudate cells;

A Kimura M., Fullki K., Nakao M.;

E TISSUE=Peritoneal exudate cells;

Kimura M., Fullki K., Nakao M.;

E Kimura M., Fullki K., Nakao M.;

T "Molecular cloning of a leukocyte integrin from the common carp.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

SR MBJJ, AB048537; BAB39135.1; -.

HSSP; P20701; 1LFA.

GO; GO:00004305; F:call adhesion receptor activity; IEA.

GO; GO:00004895; F:call adhesion receptor activity; IEA.

GO; GO:00004895; F:call adhesion; IEA.

GO; GO:00004895; F:call adhesion; IEA.

GO; GO:00004895; F:call adhesion; IEA.

DR GO; GO:0000509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00093; Integrin alpha.

InterPro; IPR00091; Integrin A; 1.

DR Ffan; PR00357; integrin A; 1.

DR Ffan; PR00357; integrin A; 1.

DR Ffan; PR00951; vwa; 1.

DR Ffan; PR00991; Int_alpha; 5.

SMART; SM00191; Int_alpha; 5.

SMART; SM00191; Int_alpha; 5.

DR FARRY; SM00191; Int_alpha; 5.
                                                                                                                                                                                                           LGTFRVMKWDNDSSNRMEIMITANSDNNGRM---SDTEVRRSVPVQFAVDLAISLVAEDS
                                          PPFPLDLSYRKVSTLQNORSQRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTF
                                                                                                                            NITEDY---DSKASLGNKLLKANVTSENNMPRTNKTEFQLELPVKYAVTMVVTSHGV-S
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
Cyprinidae, Cyprinus.
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PROSITE; PS50234; VWFA; 1.
SEQUENCE 1187 AA; 131778 MW; 85EDC7CA8B6B1C59 CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                 FSAAITSNGPLLSTVGSYDWAGGVP-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IIL 412
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U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Lymphocyte function-sesociated antigen 1 (Fragment).
Bost raurus (Bovine).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                       RIQCDIPFFGIQEEFNATLKGNL------SFDWYIKTSHNHLLIVSTABILF
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Butaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NGBI_TaxID=9606;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
E Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
E GO; CO:0008305; C:integrin complex; ISA.
GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:0004895; F:cell adhesion receptor activity; IEA.
R GO; GO:0004895; F:cell adhesion receptor activity; IEA.
R InterPro; IPR002035; WWF A.
R Ffam; PF00357; Integrin_alpha.
R Pfam; PF00357; INTEGRINA.
R Pfam; PF00357; INTEGRINA.
R PRINTS; FR00189; WFPADOMAIN.
R SMART; SM00191; Int alpha; 5.
R SMART; SM00191; Int alpha; 5.
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SEGURENCE 1086 AA; 119223 MW; FGFF2546E8C632F9 CRC64;
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Last sequence update)
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PROSITE; PS50234; VWPA; 1.
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CHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYI 1058
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                                                                                                                                                           950 RVMOHOYOV ---- SNLGORSLPISLVPLVPVRLNOTVI --- WD----RPQVTFS-ENLSST 998
                                                                                                                                                                                                                                                                                                        755 HHVKHIYQVRIQPSNYDNMP-PLEALVRVPRVHSEGLITHKWSIQMEPPVNCSPRNLESP 813
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                                                                                                                      LKANVTS-----ENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTS
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Brenan M., Rees D.J.G.;
"Sequence analysis of rat integrin alpha El and alpha E2 subunits:
"Sequence analysis of rat integrin alpha E1 and alpha E2 subunits:
tissue expression reveals phenotypic similarities between
intraepithelial lymphocytes and dendritic cells in lymph.";
EMEL, J. Immunol. 27:3070-3079[1997].
EMEL, AF022045; AAC23662.1;
HSSP; P11215; 18HQ.
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Matches 363; Conservative 213; Mismatches 464; Indels 205;
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GO; GO:0004895; F:cell adhesion receptor activity; IEA.

GO; GO:0004895; F:cell adhesion; IEA.

InterPro; IPR002035; VWF—A.

R Pfam; PF00357; integrin—A; 1.

R PRINTS; PR00145; INTEGRINA.

R SMART; SM00192; VWFADOMAIN.

R SMART; SM00192; VWFADOMAIN.

R SMART; SM00192; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 QRGGRVFIY---QKIQLERPOMVSELQGETGYPLGRFGABIAALTDINGDELIDVAVGAPE 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 DHVFQVNNFEALKTIQNQIREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLSTV 369
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                                                                                                                Thumbikat P., Kannan M.S., Maheswaran S.K.; "Sequence of the alpha subunit of bovine lymphocyte function-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 927;
                                                                                                                                                                 Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF440778; AM63636.1;

PIR; A32039; A32039.

R GO; GO:000895; P:Cell adhesion receptor activity; IEA.

GO; GO:000895; P:Cell adhesion receptor activity; IEA.

GO; GO:0007460; P:Cell-amatrix adhesion; IEA.

InterPro; IPR00413; Integrin_alpha.

InterPro; IPR00413; Integrin_alpha.

InterPro; IPR00613; WP_A.

R Pfam; PF01089; We-A.

R Pfam; PF01089; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R PROSTIE; PS0124; WHEA: 1.

R PROSTIE; PS0234; WHEA: 1.

I NON TER 927 927
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21.4%; Score 1277; DB 6; Length 9
Best Local Similarity 34.8%; Pred. No. 1e-83;
Matches 340; Conservative 167; Mismatches 385; Indels
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962 PSVMYNN--TSQSPSDHXEPFFNVHGENLFGAVFQLQICVPIXLQDF-----QIVRVKN 1013 LSST-----CHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLK 1049 GNLSPDWYIKTSHNHLLIVSTA-----EILPNDSVFTLLFQGGAFVRSQTETKVEPF-- 1101 63 NRWTAALYRCAISI-SPDEIACQ-PVEHICMPKGRYQGVTLVGNHNGVLVCIQVQARKFR 120 181 RRIVEEEDEEEDGTEIAIVLDGSGSIEPSDPQKAKNFISTWARNFYEKCFECNPALVQYG 240 194 BEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKIL 253 241 AVIQTEFDLQESRDINASLAKVQSIVQVKEVTKTASAMQHVLDNIFIPSRGSRKKALKVM 300 VVITDGEKFGDPLGYBDVIPEADREGVIRYVIGVGDAPRSEKSRQELATIASKPPRDHVF 313 QVNNFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGP-LLSTVGSY 372 361 KVINYSALDGILSKLQQRIVHMEGT---VGDALQYQLAQTGFSAQILDKGQVLLGTVGAF 417 DWAGGUFLY-TSKEKSTFINMT-RVDS-DWNDAYLGYAAAIILRNRVQSLVLGAPRYQHI 429 487 RGGOVSVCPLPRGORARWQCDAVLYGEQGPRGRFGAALIVIGDVNGDKLFDVALGAP-- 544 ----GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600 S---TRDRLREGQIQSVVIYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTC---- 712 704 SVVASEPGEREMFENPTVDVDV------TKQRQRLQCEDSSGCQSCLRKWN 748 756 749 GGSFLCEHFWLISTEEL----CEEDCFSNITIKVIYE-----FQTSGGRRDYPNFLL-D 797 757 AQRLFTALF - PPEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDS 814 856 ------POEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL--KKSKTLFSLMQYS 193 815 YRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPE 874 875 NSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTBPQLELPVKYAVYMVVTSHG 934 907 RSSVNVSVTWQLEESVFPNRTADITVTISNSNBKSLARETR---SLQFRHAFIAVLSR-- 961 935 VSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVPLVPVRLNQTVIMDRPQVTPSBN 994 ------ETLKGLPNCIBDPVSPIVLRINFSLVGTPLSAFGNLR----PVLAED SENTYVKGLCFLFGSNLRQQPQKFPEALRG 114 301 314 545 145 254 373 199 713 66666 දු පු ò Ď 8 8 8 8 6 8 6 d 요 셤 입 8 ò රි සි රි පි ජි ò 셤 \$ 8

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	Integrin alpha 82 (Pragment). Rattus norvegious (Rat)
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5 E	NCBI_TAXID=IVII6; [1]
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X	MEDLINE=98056820; PubMed=9394838;
5 2	integrin a
RT	nenotypic similarities between
	intraepithelial lymphocytes and dendritic cells in Lymph."; Dir .T Temmod 27.3070.2070/1907)
	EMIL: 0. IMMUNICI. 27:30/0-30/3/L237/. EMBL: AF020046: AAC23663.1:
置	HSSP, P11215; 1BHQ.
	GO; GO:0008305; C:integrin complex; IBA. CO: CO:000490E: R:cell adhesion recentor activity: IRB
	InterPro; IPR000413; Integrin_alpha.
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8 8	PRINTS; PR01185; INTEGRINA.
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ž E	PROSITE; PSSU234; VWFA; I.
80	SEQUENCE 1167 AA; 128593 MW; B3FED7E18B5CBBEC CRC64;
Bee	atch 18.9%; Score 1125.5; DB 11; Length 1167; cal Similarity 27.8%; Pred No. 1.6e-72;
	2; Conservative 214; Mismatches 456; Indels 243; Gaps
à	5 VLLITALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY 64
og Q	ASLKPLGAFN
à	65 QCDYSTGSCEPIRLQVPVEAVNM-SLGLSLAATTSPPQLLACGPTVH 110
qq	44 QDPSNNQTCLLVARRSSNRNSAVLYQCATSIIPDEIGCQPVEHILMPKGRYQGVTL 99
à	111QTCSENTYVKGLCFLFGSNLRQQPQKFPEALRG 143
a a	100 VRNHNGVLVCIQVQSRKPRSLNSELTGACSLLTPNLDLQAQAYPSDLEGVLDLGASVNSG 159
Š	144CPOEDSDIAFLIDGSGSIIPHDFRRMKEFVS 174
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9	DIIGSNGGSIGEEINSAKKLKKYAVEEEDEERGIEIAIVLUGSGSIEFSUFQAANUFIS 21
à	175 TVMEQLKKSKTLFSLAQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIR 232
qq	mrnfyekcfecnfalvoyggviqtefdlidsrdinaslakvosivovkevikiasa
Š	233 KVVRELPNITNGARKNAFKILVVITDGBKFGDPLGYEDVIPBADREGVIRYVIGVGDAFR 292
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           397 TGFSAQILDKGQVLLGTVGAFNWSGGALLYNTQNGRGRFLNQT-AKEDFRAAQYSYLGYS
                                                                                                               YYRGMSVSGSLDFSGDDLADITVGSQDVAVVLRSRPVVDLTVSMTFTFDALP-----
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                                                                                                                                       LGDVNGDKLTDVALGAP-----GREDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRL
                                                                                                                                                  QVVKGKEAGEVRVCLHVQKS---TRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNS
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SEKSROELNTIASKPPRDHVFOVNNFBALKTIONQLREKIFAIEGTOTGSSSSFEHEMSO
                                EGPSAAITSNGP-LLSTVGSYDWAGGVFLY-TSKEKSTFINMTRVDSDMNDA---YLGYA
                                                                                                     SNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGBQGQPWGRFGAALTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAASYWMLTALFHLIGASNVDVKNAMTFSGPLEDMFGYTVQQYENEEGKWVLIGSPLVGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVIGVGDAF-----RSEKSROELNTIASKPPRDHVFQVNNFBALKTIQNQLREKIFAIEG
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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ilarity 28.4%; Pred. No. 2.3e-68;
Conservative 215; Mismatches 521; Indels 145; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      "Smooth muscle cell phenotype-dependent transcriptional regulation the alphal integrin gene.";
The alphal integrin gene.";
Taiol. Chem. 27:226643-2651(1997).
BMBL; AB000470; BAA23160.1; -.
BMBL; AB000471; BAA23160.1; -.
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Mobin W. 197476270; PubMed=9334246;
Mobin H., Hayashi K., Nishida W., Momiyama T., Uchida A.,
Sobue K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1171 AA; 130228 MW; B505A4D65F09736B CRC64;
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PROSITE; PS50234; VWFA; 1.
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                                                                                                                                               NCBI_TaxID=9031;
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Matches 349;
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Search completed: June 7, 2004, 17:16:09 Job time: 48.0446 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                   Copyright
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OM protein - protein search, using sw model

June 7, 2004, 16:54:39; Search time 50.1568 Seconds (without alignments) 6495.175 Million cell updatés/sec Run on:

US-09-902-481B-1 5956 1 MALRVLLLTALTLCHGFNLD.....FKRQYKDWMSEGGPPGAEPQ 1153 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:*

1. geneseqp1980s:*

2. geneseqp2000s:*

4. geneseqp2001s:*

5. geneseqp2001s:*

6. geneseqp203as:*

7. geneseqp203as:*

8. geneseqp2003as:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STUMMENTES

	Description	Aaw65090 Human Bet	Aab07360 Human CD1	Aau80252 Human int	Abg61469 Human Bet		Add25615 Binding d	Aar04136 Alpha sub	Aar07120 p150.95 a	Aaw65091 Human Bet	Aab07361 Human CD1	Abg61470 Human Bet	Abu07406 Protein d	Aar78166 Human bet	Aaw23049 Human bet	Aaw57491 Human bet	Aaw65089 Human Bet	Aaw72825 Human alp	Human	Aab07359 Human alp	Abg61468 Human Bet	Aaw23064 Human bet	Aaw65106 Human Bet	Aaw72837 Human alp	Human	Aab07376 Human alp
SUMMARIES	ID	AAW65090	AAB07360	AAU80252	ABG61469	AA014428	ADD25615	AAR04136	AAR07120	AAW65091	AAB07361	ABG61470	ABU07406	AAR78166	AAW23049	AAW57491	AAM65089	AAW72825	AAW73342	AAB07359	ABG61468	AAW23064	AAW65106	AAW72837	AAW73343	AAB07376
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de	Query Match	6	100.0	100.0	100.0	100.0	100.0	8.66	58.7	58.4	58.4	58.4	58.4	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	57.7	57.7	57.7	57.7	57.7
	Score	5956	5956	5956	5956	5956	2956	5946	3494	3480	3480	3480	3478	3455	3455	3455	3455	3455	3455	3455	3455	3439.5	3439.5	φ.	3439.5	3439.5
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Abg61485 Human Bet Aar78169 Rat alpha Aav33062 Rat beta Aav60004 Rat alpha		Aaw23061 Mouse bet Aaw60003 Mouse alp Aaw65103 Mouse bet	Aaw72836 Mouse alp Aaw73347 Mouse alp Aab07373 Mouse alp	Abg61482 Mouse Bet Aaw65104 Rat beta- Aaw73345 Rat alpha	Aar78168 Mouse alp Aav3059 Kat beta Aav60001 Rat alpha Aav65101 Rat beta-
ABG61485 AAR78169 AAW23062	AAM72824 AAB07374 ABG61483	AAW23061 AAW60003 AAW65103	AAW72836 AAW73347 AAB07373	ABG61482 AAW65104 AAW73345	AAR78168 AAW23059 AAW60001 AAW65101
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2220	3333	3 3 3 5 4 5	36 337 38	39 4 40 11	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA. (first entry) 28-SEP-1998 AAW65090; RESULT 1 aaw65090

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis.

Homo sapiens

US5728533-A.

95US-00485618. 07-JUN-1995; 17-MAR-1998.

93US-00173497. 94US-00286889. 94US-00362652. 23-DEC-1993; 05-AUG-1994; 21-DEC-1994;

(ICOS-) ICOS CORP.

Van Der Vieren M, Gallatin WM;

WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CDILb subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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 diseases such as type-I diabetes, atherosclerosia, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
                                                                                                                                                                                          GLCFLFGSNIRQQPQXFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 180
                                                                                                                                                                                                      GLCFLFGSNLRQQPQXFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQL 180
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                                                                                                                                                                                                                                    KKSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLVXPITQLLGRTHTATGIRKVVRELFN
                                                                                                                                                                                                                                                KKSKTLPSLMQYSEBFRIHFTPKEPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRBLFN
                                                                                                                                                                                                                                                                                      361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
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                                                                                                      1 MALRVILLTALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
                                                                                                                                                                                                                                                                            ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL
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                                                                                      Gaps
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                                                                DB 2; Length 1153;
                                                                                    Indels
                                                                                 9;
                                                              Query Match

100.0%; Score 5956;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1153; Conservative 0; Mismatches
                                            Sequence 1153 AA;
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta? subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta? integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit: alpha (AAA60014 and AAB07159). The present sequence has subunit: alpha (AAA60014 and AAB07159). The present sequence has subunit: alpha dientity to the protein sequence of alpha d. The Alpha dene and protein may be useful in therapy for diseases linked to aberrant alpha dienction e.g. Type I diabetes, atherosclerosis, multiple cielerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
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                                                                                                                                                                   TLIPGQAAFVRSQIEFKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
IGORSLPISLVPLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                    1021 VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immunosuppressive activities. The polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-I antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease,
                                                           1081 TLLPGQGAFVRSQTETXVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFPKRQYKD
1081 TLLPGQGAFVRSQTETKVBPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKD
              LGQRSLPISLVPLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                             Modified integrin-I or integrin I-like domain polypeptide useful as immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired conformation.
                                                                                                                                                                                                                                                                                                                                          Integrin, antiinflammatory; imunosuppression; nephritis; de:
inflammatory disease; autoimmune disorder; Crohn's disease;
human immunodeficiency virus; HIV; mycoardial infarction;
Sjorgen's syndrome; rheumatoid arthritis.
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                                                                      Length 1153,
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inhibition of macrophage infiltration at the site system injury. The monoclonal antibodies can also diagnose Crohn's disease
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100.0%; Score 5956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches
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nephritis; human immunodeficiency virus (HIV), myocardial infarction, Sporgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-1 alpha-M protein subunit used to generate the mutant polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-R or VCBM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following
                                                                                                                                           961 LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKADV
                                                                                                                                                                                                  VNCSIAVCORIOCDIPPEGIOEEPNATIKGNISFDWYIKTSHNHILIVSTABILENDSVF
                                                             NUTSENNMPRINKTEPQLELPVKYAVYMVYSHGVSTKYLNFTASENTSRVMQHQYQVSN
                                                                                                                                                                                                                                           1021 VNCSIAVCQRIQCDIPFFGIQESFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Beta2 integrin alphaCD11b subunit.
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spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphab crows and proteins, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as IAD [leukocyte adhesion deficiency, inflammatory response, diabletes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative complex, immune complex alvolitis and leukaemia. The present sequence is Beta2 integrin alphab protein sequences 88888888888888

Sequence 1153 AA;

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780 120 120 180 180 240 240 300 300 NTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360 360 420 420 480 480 540 540 900 900 999 999 720 720 780 840 840 9 9 GLCFLFGSNLRQOPOKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMRQL KKSKTIPSLAQYSEEPRIHFTFKEFQNNPNPRSLVKPITQLLGRIHTATGIRKVVRELFN NTIASKPPRDHVFQVNNFBALKTIQNQLREKIFAIBGTQTGSSSSFEHENSQBGFSAAIT STRDRLRBGQIQSVVTYDLALDSGRPHSRAVFNBTKNSTRRQTQVLGLTQTCBTLKLQLP NCIEDPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEXNCGNDNICQDD 1 MALRVILLTALITACHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR GSLYQCDYSTGSCEPIRLQVPVEAVNWSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL ITNGARKNAFKILVVITDGEKFGDPLGYEDVI PRADREGVIRYVIGVGDAFRSEKSRQEL LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV DLTVGAQGHVLJLRSQPVLRVKAIMBFNPREVARNVFBCNDQVVKGKEAGEVRVCLHVQK MALRVLLLTALTLCHGFNLDTENAMTPQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR KKSKTLPSIMQYSEBPRIHFTPKBPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN SNGPLLSTVGSYDWAGGVPLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV Gaps Ċ. Length 1153; Indels 5, ö 13 100.0%; Score 5956; 100.0%; Pred. No. 0; 0, Mismatches Conservative Best Local Similarity Matches 1153; Conserv 541 601 181 241 421 541 661 721 781 61 61 121 121 181 301 361 361 481 481 601 199 721 241 301 421 Query Match

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1080 VNCSIAVCQRIQCDIPFFGIQBEFNATLKGNLSFDWXIKTSHNELLVSTABILFNDSVF 1080 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140 900 Mac-1; integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related immunological disorder; rheumatoid arthritis; ischaemia, reperfusion; hypovolemic shock; infarction; cerebral shock; varial infection; cancer; gene therapy; vaccine; VNCSIAVCQRIQCDIPFFGIQBEPNATLKGNLSPDWYIKTSHNHELIVSTAEILFNDSVF NVTSENNMPRTNKTEPOLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMOHQYQVSN LGORSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV ORSWILACES ASSTEVSGALKSTSCS INHPIFPENSEVIFNITFDVDSKASLGNKLLLKA New integrin I domain protein having alteration in at least 2 noncontiguous regions and exits in an open conformation, useful for treating, preventing or suppressing inflammatory or immunological disorders. (CALY) CALIFORNIA INST OF TECHNOLOGY (BLOO-) CENT BLOOD RES. Ź Example 1; Fig 1F; 90pp; English. AAO14428 standard; protein; 1153 Integrin Mac-1 alpha subunit. 09-JUL-2001; 2001WO-US021805. 07-JUL-2000; 2000US-0216600P. MMSEGGPPGAEPQ 1153 bioactive agent screening WPI; 2002-148167/19. (first WO200204521-A2. Unidentified 17-JAN-2002. 03-MAY-2002 Springer T; 1081 841 1021 1021 1081 1141 AA014428; 901 901 961 961 1141 841 RESULT 5
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The invention comprises structurally biased variant integrin inserted (1) domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins.

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The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatorid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating: ischaemial infection; and cancer. The variant integrin I domain infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for bloactive agents. The present amino acid sequence represents the Mac-1 alpha subunit of integrin
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Matches 1153, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                     TLLPGQGAFVRSQTETKVEPFBVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
                                             NVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN
                                                              NVTSENINIPRITIKTEFQLELPVKXAVYAVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN
                                                                                                                                                                 VNCSIAVCQRIQCDIPPFGIQBEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVF
                                                                                                                                                                                    VNCSIAVCQRIQCDIPPFGIQEBFNATLKGNLSFDWYIKTSHNHELIVSTABILFNDSVP
                                                                                                                                                                                                                           TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFPKRQYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; (TH2 constant region; CH3 constant region; 1961; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixa malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding domain-immunoglobulin fusion protein-associated protein
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                                                                                                                                       1141 MMSEGGPPGARPQ 1153
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thinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide; derived from (a) having 3 or more cysteline residues; where the first cysteline residues; where the first cysteline is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains to more than one cysteline residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteline residue; and a wutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteline residue; he binding domain immunoglobulin hinge region polypeptide contains no cysteline residues. The binding domain immunoglobulin hinge region polypeptide contains no cysteline residues to mimmunoglobulin hinge region polypeptide contains no cysteline residues. The binding domain immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region polypeptide contains no contains no contains no cysteline residues the polymucleoticity (ApCC) and complement fixation. The binding domain immunoglobulin fusion protein, a recombinant expression construct, comprising the polymucleotide (operably linked to a promoter), a host rocluded are an isolated polymucleotide with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a construct, producing the binding domain-immunoglobulin fusion protein or suspected of having a malignant condition or a B-cell disorder, thaving or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, mutation and sease. The present sequence is a binding domain immunoglobulin fusion protein sequence data for this patent formed part of the printed specification by their SeQ or autoimmune sequence. The presence data for this patent formed specification by their SeQ or unwher therefore none of the sequences can be explicitl

Sequence 1153 AA;

300 GSLYQCDYSTGSCEPIRLQVPVEAVMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120 KKSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRBLFN 240 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN 240 NTIASKPPRDHVFQVNNFEALKTIQNQLRBKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360 360 SNGPLLSTVGSYDWAGGVPLYTSKÆKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420 9 9 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGGSVVQLQGSRVVVGAPQEIVAANQR NTIASKPPRDHVPQVNNFBALKTIQNQLREKIFAIRGTQTGSSSSFEHEMSQEGFSAAIT MALRVILLITAL TLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR ITNGARKNAPKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL Gaps ô Query Match
100.0%; Score 5956; DB 7; Length 1153;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 0; Indels 0; н 61 241 241 301 301 61 181 181 361 361 421 421 g qq СD 셤 ద ò g ò g ઠ à ઠે Š ठे ઠે

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481 HYYEÇTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA :	541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV (601 DLTVGAQGHVILLESQPVLRVKAIMEFNPREVARNVFECNDQVVKGKBAGEVRVCLHVQK	61 STRDRLRRGGIOSVVTYDLALDSGRPHSRAVFNRTRKNSTRRQTQVLGLTQTCETLKLQLP	21 KUBERREGIGSVVIIDAALOSGREGSKAVENEINNSIKRKIQVESTIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIG	1 NCIEBPEVSFIVLRINFSLVGTPLSAFGRILFPVABDAQRIFTALFPFERNCGNDNICQDD .	781 LSTTPSFMSLDCLVVGGPRERVITYPRNDGEDSYRTOYTFFPELDLSYRKYSTLONGKS [841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKA.	901 NVTSENMMETHKTEPOLELEVKYAVYMVVTSHGVSTKYLNFTASENTSRVMOHOYQVSN 901 NVTSENNMFRTHKTEPOLELEVKYAVYMVVTSHGVSTKYLNFTASENTSRVMOHOYQVSN	961 LGGRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELEKAPV 	1021 VACSIAVCQRIQCDIPFFGIQBERNATLKGNLSFDWYKTSHNFLLIVSTARILFNDSVF 1021 VACSIAVCQRIQCDIPFFGIQBERNATLKGNLSFDWYKTSHNFLLIVSTABILFNDSVF	081 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSWGGLLLLALITAALYKLGFFKRQYKD	1 ILLEGGERGEPROQUELTAVERFEVENETETAVGSSVGGELELERLITARLITARLITARLITAGERANGING. 1 MMSEGGERGEPG 1153	141 MMSEGGPPGAEPQ	14136	CAR-	pha subunit of Mac-1 leukocyte adhesion receptor.	-1 alpha subunit; Mac-1 alpha/beta heterodimer; -specific defence system; integrin gene superfamily.	thetic.	Location/Qualifiers	/label= signal peptide fied-site 9689	fied-site 240242 /label= putative N-glycosylati fied-site 391393
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                           NTIASKPPRDHVFQVNNFFALKTIQNQLREKIPAIGTQTGSSSFEHEMSQEGFSAAIT
                                                                                                                GSLYQCDYSTGSCEPIRLOVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
            NTIASKPPRDHVPQVNNFEALKTIQNQLRBKIPAIEGTQTGSSSSFEHEMSQEGFSAAIT
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                                                                                                                                                                                                                                                                                                                 Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MRR-2003 to correct PR field.) (Updated on 29-MRR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                         treating
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New pure Mac-1 alpha sub-unit and corresp. DNA - useful inflammation and viral infections, and in diagnosis.
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Pred. No. 0;
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89US-00321239.
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Matches 1152; Conservative (
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Treatment of viral esp. rhino-viral infection - by admin. of alpha sub-
unit of p150.95 cell surface adhesion receptor, opt. together with a beta
chain of CD-18 family.
                                                                                                                                   cell leukaemia;
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                                                                                                                          p150,95 leucocyte adhesion receptor alpha-subunit; hairy rbinovirus.
                                                                                                                  p150.95 alpha subunit encoded by clone lambdaX47
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probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it intracts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAQ06068, AAR07121-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                              Length 1163;
                                                                             Query Match 58.7%; Score 3494; DB 2;
Best Local Similarity 61.2%; Pred. No. 4e-282;
Matches 698; Conservative 138; Mismatches 299;
                                                                Sequence 1163 AA;
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Sequence 1163 AA;

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                                                                                                          BINT PRISKTTFQLELPVKYAVTUVSSHQFTKYLNFSBSEEKBHVANGHRYQVINLGQ
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ENNMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTAS-
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AAB07361 standard; protein; 1163 AA

(first entry) 17-JAN-2001 AAB07361;

Human CD11c protein sequence

Human; macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAV; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoic arthritis; central nervous system injury; CDllc.

Homo sapiens

WO200029446-A1

25-MAY-2000

99WO-US027139 16-NOV-1999; 98US-00193043 99US-00350259 16-NOV-1998; 08-JUL-1999;

CORP. (1COS-) ICOS Van Der Vieren Gallatin MW,

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WPI; 2000-387751/33

novel anti-alpha integrin d monoclonal antibodies to inhibit hage infiltration and reduce inflammation at central nervous system injury sites. Use of

Example 5; Fig 1; 270pp; English

Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins con an important role in immune and inflammentory responses. The present cor protein sequence is the human integrin alpha subunit CD11c. This sequence was used in an alignment to identify a novel beta2 integrin alpha comproximately 66% identity to the protein sequence of alpha d. The capproximately 66% identity to the protein sequence of alpha d. The chipha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple confirms in addition, anti-alpha d monoclonal antibodies may be used in the inhibition of macrophage infilitation at the site of a central nervous system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease

Ą Sequence 1163

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294; Indels

Length 1163;

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58.4%; Score 3480; D llarity 61.1%; Pred. No. 6e-2 Conservative 144; Mismatches

al Similarity 697; Conserv

Query Match Best Local Matches 69

RSLPISLVFLVPLVPVRLNQTVIMDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVANC 1023 485 963 305 364 365 424 425 484 544 544 604 604 664 664 724 724 784 784 844 844 904 902 124 184 185 244 304 127 67 845 HLTC--CSAPVGSQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVGLDRLLLIANVSS BNNIPRTSKTIFQLELPVKYAVYIVVSSHEQPTKYLNFSESEEKESHVAMHRYQVNNLGO QCDYSTGSCRPIRLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCP ARKNAFKILVVITDGEKFGDPLGYEDVIPBADREGVIRVVIGVGDAFRSEKSRQELNTIA 246 ARRDAIKILIVITDGKKEGDSLDYKDVIPWADAAGIIRYAIGVGLAFQNRNSWKELNDIA SKPPRDHVPQVNNPEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGP **<u>OTRGGOVSVCPLPRGORARWOCDAVLYGBOGOPWGRFGAALTVLGDVNGDKLTDVAIGAP</u>** GAQGHVI.LLRSQPVI.RVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD RLREGOIQSVVTYDLALDSGRPHSRAVFNETKNSTRROTQVJGLTQTCBTLKLQLPNCIE DPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT FS FMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFFLDLSYRKVSTLQNQRSQRSW ENNMPRINKTEFQLELPVKYAVYMVTSHGVSTKYLNFTAS-ENTSRVMOHQYQVSNLGQ LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK LLSTVGSYDWAGGVFLYTSKEKSTFINYTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAA RYOHIGLVAMPRONTGMMESNANVKGTOIGAYPGASLCSVDVDSNGSTDLVLIGAPHYYE GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS TLPSLMQYSBEFRIHFTFKEPQNNPNPRSLVXPITQLLGRTHTATGIRKVVRBLFNITNG VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLX 245 306 426 545 605 599 665 725 785 845 185 365 425 485 725 785 905 903 964 ß ω 128 305 65 68 125 a ద ò ద Š 셤 ઠે 셤 ठे 영 음 셤 ઠે ď <u> የ</u> ઠ g 8 ď Š 셤 .qq 요 ਨੇ à g ò ò 쉱 ò

The invention relates to promoting locomotor recovery, inhibiting an locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a nati-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a nati-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-R or VCAM-I (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphab con a minital and conditions are also useful for are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; infracellular cell adhesion molecule; vascular cell adhesion molecule; autonomic dysfunction; sensory dysfunction; spinal cord injury. Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. RDLPVSINFWVPVELNQEAVWMDVBVSHPQNPSLRCSSEKIAPPASDFLAHIQKNPVLDC SIAVCORIOCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL PGQGAFVRSQIBIKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS Human Beta2 integrin alphaCD11c subunit. Example 5; Page 194-198; 270pp; English ABG61470 standard; protein; 1163 AA. Vieren M; 15-OCT-2001; 2001WO-US032059. 13-OCT-2000; 2000US-00688307. (first entry) Van Der WPI; 2002-463260/49. CORP. E 1144 Ë 1143 WO200230980-A2 sapiens (100S-) ICOS Gallatin WM, 27-AUG-2002 18-APR-2002. 1023 1084 1144 1143 963 Homo g ठ े 음 à 쉱

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colitis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the Beta2 integrin alphaD protein sequences
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises concer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves certaining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Or fraget genes which are differentially-regulated in prostate cancer. Or fraget genes which are differentially-regulated in prostate cancer contivity of a polypeptide differentially-regulated in prostate cancer calls, which involves contacting a polypeptide differentially-regulated contacting a polypeptide differentially defined activity of the test agent markers abiological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, grading, assessing, monitoring, prognosticating.
                                1022
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                                                                                                                                                         Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
               PGQCAFVRSQTETKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDNMS
RSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKRRLPSHSDFLAELRKAPVVNC
                                                                    SIAVCORIOCDIPPEGIQESFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein differentially regulated in prostate cancer #9.
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Cronditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer c. e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide. (I) is useful con the rappeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways (C) physiologically relevant to prostate cancer permits the definition of the functional and disease pathways and the delineation of targets in these cancer may be addinguised to targets in these captures. This is the anion acid sequence of a protein differentially regulated in prostate cancer.
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465. 474
700te= "putative cation binding 518. 527
7note= "putative cation binding
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/note= "extracellular domain"
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CH11a,b,c and may be a site f
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'note= "transmembrane region'
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/note= "cytoplasmic domain"
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natory bowel disease; asthma
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A probe based on a partial cDNA clone (given in AAQ91727) of canine alpha -TM1 was used to screen a human spleen cDNA library to identify clone 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d. The cDNA was manigulated to allow expression of recombinant alpha-d subunit in COS and CHO cells
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                                                                                      - used to
of graft
                                                                                                                                                                                                                                                                                                                                                        Length 1161;
                                                                                      Alpha sub-unit polypeptide of human beta 2 integrin - used potential antiinflammatory agents, for the treatment of granteriosclerosis, inflammatory bowel disease, asthma, etc.
                                                                                                                                                                                                                                                                                                                                                           Query Match 58.0%; Score 3455; DB 2; Length 1
Best Local Similarity 59.9%; Pred. No. 7.4e-279;
Matches 684; Conservative 162; Mismatches 287; Indels
                                                                                                                                                                      Claim 7; Page 82-87; 172pp; English
Van Der Vieren M;
                                  WPI; 1995-240603/31.
N-PSDB; AAQ91712.
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                                                                                                                                                                                              1078 PGQEAFWRAQMEMVLEEDBVYNAIPIIMGSSVGALLLLALJTATLYKLGFFKRHYKEMLE 1137
                                                                                                                          RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNC 1023
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                                                                     ENNMPRTNKTEPQLELPVKYAVYMVVTSHGVSTKYLNF-TASENTSRVMQHQYQVSNLGQ
DPVSPIVLRLNPSLVGTPLSAFGNLRPVLABDAQRLFTALFPFEKNCGNDNICQDDLSIT
        DVVSPIILHINPSLVREPIPSPQNLRPVLAVGSQDLFTASLPFERNCGQDGLCEGDLGVT
                              FSFMSLDCLVVGGPREFNVTVTVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW
                                                             RLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTS
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|abel= Transmembrane domain
note= "homologous to the human CD11c transmembrane
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'label= Cytoplasmic_domain
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                                                                                                                Hybridoma 199M and antibody secreted by it - specific for new rat beta2 integrin subunit, useful to detect subunit in cells and modulate its activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VILLITALTLCHGFNLDTENAMTFQBNARGFGQSVVQLQGSRVVVGAPQBIVAANQRGSLX
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al Similarity 59.9%; Pred. No. 7.4e-279;
684; Conservative 162; Mismatches 287; Indels
                                                                                                                                                                                                                   Example 5; Page 116-120; 222pp; English
Der Vieren M;
                                              WPI; 1997-435154/40
Van
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                                                                      N-PSDB; AAT79220
Gallatin WM,
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                                                                                                                                                                                                         PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS 1143
                                                                                                                                                                                                                                        RSLPISLVFLVPVRLAQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023
604 GARGQVLLLRSLPVLKVGVAMRFSPVBVAKAVYRCWEEKPSALEAGDATVCLTIQKSSLD 663
                                                     DVVSPIITHENPSLVREPIPSPQNERPVLAVGSQDLFTASLPFERNCGQDGLCEGDLGVT 781
                                                                          FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW 844
                                                                                    RLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTS 904
                                                                                                                842 REACETV-PTEDEG-LRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATIGDRAHMRASAES 899
                                                                                                                                      ENNMPRINKTEFQLELPVKYAVYMVTSHGVSTKYLNF-TASENTSRVMQHQYQVSNLGQ 963
                                                                                                                                             DPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT 784
                                                                                                                                                                                                                                                                                                                                                                           Beta 2 integrin alpha subunit; alpha d; human; treatment; diabetes; reporter-transactivator construct; arteriosclerosis; atherosclerosis; inflammatory bowel disease; arthritis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                             Human beta2 integrin alpha subunit (alpha d) polypeptide.
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/note= "extracellular domain"
150. 352
/note= "I (insertion) domain"
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/note= "transmembrane region"
1129. .1161
/note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mature protein"
                                                                                                                                                                                                                                                                                                                 AAW57491 standard, protein; 1161 AA.
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This represents a human beta2 integrin alpha subunit (alpha d)

polypeptide. This is used in the methods of the invention for isolating a polypeptide. This is used in the methods for the invention for isolating a polymuctoride encoding a protein that binds to alpha d. The method comprises transforming or transfering host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and activating domain. A first hybrid DNA sequence encoding a fusion of at least part of alpha d and either the DNA-binding domain or the activating domain of the transcription factor and a library of hybrid DNA sequences encoding tissions of at least part of putative alpha d-binding proteins and the DNA binding domain of the transcription factor which is not incorporated in the first fusion are expressed in the host cells. The binding of an alpha d-binding protein to alpha d in a particular host cell is detected by determining production of the reporter gene product in the cell. The hybrid DNA sequence encoding the alpha d-binding protein can be isolated from the cell. Alpha d may be useful for treating graft arteriosclerosis, aberosclerosis, diabetes, useful for treating graft arteriosclerosis, aberosclerosis, diabetes,
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                                                                                                                                                                                                                                                                                                                                                                                      isolation of DNA encoding protein that binds to integrin subunit recombinant cells containing reporter-transactivator construct.
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Best Local Similarity 59.9%; Pred. No. 7.4e-279;
Matches 68%; Conservative 162; Mismatches 287; Indels
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                                                                                                                                                                                                                          Van Der Vieren M, Gallatin WM,
94US-00362652.
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21-DEC-1994;
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                                                                                  ENNMERTHKTEFQLELFVKYAVYMVVTSHGVSTKYLNF-TASENTSRVMQHQYQVSNLGQ 963
                                                                                                                                                                                                          PSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW 844
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2: /cgn2_6/ptodate/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodate/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodate/1/pubpaa/USO6_NEW_PUB.pep:*

6: /cgn2_6/ptodate/1/pubpaa/USO6_NEW_PUB.pep:*

6: /cgn2_6/ptodate/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodate/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodate/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodate/1/pubpaa/USO9_NEW_PUB.pep:*

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15: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodate/1/pubpaa/USO8_NEW_PUB.pep:*

18: /cgn2_6/ptodate/1/pubpaa/USO8_NEW_PUB.pep:*

19: /cgn2_6/ptodate/1/pubpaa/USO8_NEW_PUB.pep:*

19: /cgn2_6/ptodate/1/pubpaa/USO8_NEW_PUB.pep:*

19: /cgn2_6/ptodate/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1155919 segs, 281338677 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3, Appli	Sequence 1, Appli	Sequence 3, Appli	30,	Sequence 176, App	Sequence 4, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 204, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Segmence 2. Appli
	. QI	US-09-350-259-3	US-09-902-481A-1	US-09-891-943-3	US-10-144-259-30	US-10-207-655-176	US-09-945-265-4	US-09-902-481A-6	US-09-902-481A-5	US-09-902-481A-4	US-09-902-481A-3	US-10-116-275-204	US-09-350-259-4	US-09-891-943-4	US-09-350-259-2	TIS-09-891-943-2
		. 6	10	10	14	14	<u>σ</u>	10	10	10	10	15	σ	10	σ	Ċ
	Query Match Length DB	1153	1153	1153	1153	1153	1152	1137	1137	1137	1137	1163	1163	1163	1161	1161
dio	Query Match	100.0	100.0	100.0	100.0	100.0	7.66	98.5	98.4	98.3	98.0	58,8	58.4	58.4	58.0	0.00
	Score	5956	5956	5956	5956	5956	5940.5	5868	5862	5852	5839	3503	3480	3480	3455	3455
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90	Sequence 33, Apply	'n	41	Sequence 53, Appl	Sequence 53, Appl	Sequence 37, Appl	Sequence 37, Appl		Sequence 46, Appl	Seguence 1212, Ap	Sequence 2, Appli	۳	Sequence 295, App				2,	Sequence 101, App	ď	ď	25	Seguence 810, App	2	2	Seguence 338, App	35	Sequence 35, Appl	Sequence 4, Appli	Sequence 187, App
US-09-350-259-99	1947147017	US-09-350-259-55	US-09-891-943-55	US-09-350-259-53	US-09-891-943-53	US-09-350-259-37	US-09-891-943-37	US-09-350-259-46		US-10-087-192-1212	US-09-945-265-2				US-09-350-259-103	US-09-891-943-103	US-09-350-259-101		US-10-177-550-2			US-1	ns-	-SD		09-984-1	US-09-836-353A-35	US-10-262-839-4	US-10-211-462-187
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57.7			54.9	54.8	54.8	54.6	54.6	54.4	54.4	31.0	26.2	26.2	25.8	22.9	20.6	20.6	20.0	20.0	19.5	19.5	18.9	18.6	18.6	18.6	18.6	18.5	18.5	18.5	18.3
3439.5	J. V. C.	3270.5	3270.5	3264	3264	3251.5	3251.5	3243	3243	1848	1563	1559	1535.5	1361	1229.5	1229.5	1189.5	1189.5	1163	1163	1123.5	1110	1108.5	1108.5	1106	1102.5	1102.5	1102.5	1087.5
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ALIGNMENTS

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61 GSLYQCDYSTGSCEPIRLQVPVEAVNMSIKILSLABATTSPPQLLACGPTVHQTCSENTYVK 120
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                                                                                      GERERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVEXTION: NO. US20020062008Alel Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER PILING DATE: 1999-11-23
EARLIER PILING DATE: 1999-06-05
EARLIER PILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN Ver. 2.0
ERVINDE: PALENTIN VER. 2.0
ERVINDE: PALENTIN VER. 2.0
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Conservative 0; Mismatches
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US2002062008A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-350-259-3
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                               GECFLFGSNLRQQPQKPPBALRGCPQBDSDIAFLIDGSGSIIPHDFRRMKBFVSTVMBQL 180
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US-09-902-481A-1

Sequence 1, Application US/09902481A

Publication No. US20030054440A1

GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE PEPERENCE: A-70586-1/RFF/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2000-07-09

PRIOR FILING DATE: 2000-07-09

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO: 10-07-09
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: mat_peptide
LOCATION: (17)..()
OTHER INPORMATION:
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us-09-902-481b-1.rapb

MALRYLLITALTLCHGFNLDTENAMTFOENARGFGGSVVQLGGSRVVVGAPQEIVAANGR MALRYLLITALTLCHGFNLDTENAMTFOENARGFGGSVVQLGGSRVVVGAPQEIVAANGR G1 GSLYQCDYSTGSCEDFIRLQVPVEAVAMSLGLSLAATTSPPQLLACGFTVHQTCSENTYVK G1 GSLYQCDYSTGSCEDFIRLQVPVEAVAMSLGLSLAATTSPPQLLACGFTVHQTCSENTYVK Qy 121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRENKEFVSTVMEQL Db 121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRENKEFVSTVMEQL Qy 181 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKDITQLLGRTHTATGIRKVVRELFN Db 181 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKDITQLLGRTHTATGIRKVVRELFN Qy 241 ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPRADEGCVIRTUGGDAFRSEKSRQEL Db 241 ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPRADEGCVIRTUGGDAFRSEKSRQEL OY 301 NTIASKPPRDHYPQVNNFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT Db 311 NTIASKPPRDHYPQVNNFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT DD 311 NTIASKPPRDHYPQVNNFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT DD 311 NTIASKPPRDHYPQVNNFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT	0 0 0 36 0 42 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Db 481 HYYEGTRGGQVSVCPLPRGGRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA	661 STRDRIABGOLOSVYTYDLALDSGRPHSRAVFNETRNS	Db 791 LSITESFMSLDCLVVGGPREFNYTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS OY 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA Db 841 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA OY 901 NYTSENNMFFTINKTEFQLELPVKXAVXTVAVTSHGVSTKXLNFTASENTSRVMQHQYGNSN Db 901 NYTSENNMFFTINKTEFQLELPVKXAVXTWVTSHGVSTKXLNFTASENTSRVMQHQYGNSN DD 901 NYTSENNMFFTINKTEFQLELPVKXAVXTWVTSHGVSTKYLNFTASENTSRVMQHQYGNSN	KERLPSHSDFLAELRK 	D D 7
OUTUGAQCHVILLESQPVIRVXAIMEFNDREVAENVFECNDQVVKGKEAGEVRVCLHVQK 660	960 102 102 108 108		US-09-891-943-3) Sequence 3, Application US/09891943) Publication No. US2030077278A1) Publication No. US2030077278A1) APPLICANT: Gallatin, Michael W.) APPLICANT: Gallatin, Monica TITLE OF INVENTION: No. US2030077278A1el Human 2 FILE REPERENCE: 27866/35004 CURRENT APPLICATION NUMBER: US/09/891,943	CURRAIL FILING DATE: 2001-06-26 PRIOR PLING DATE: 1998-11-16 PRIOR FILING DATE: 1998-11-16 PRIOR APPLICATION NUMBER: 08/286,889 PRIOR APPLICATION NUMBER: 08/362,652 PRIOR PLING DATE: 1994-08-05 PRIOR PLING DATE: 1994-12-21 PRIOR PLING DATE: 1997-10-03 PRIOR PLING DATE: 1997-10-03 PRIOR PLING DATE: 1997-10-03 PRIOR PLING DATE: 1997-10-03 NUMBER OF SQL ID NOS: 114	; SEQ ID NO 3 ; LENGTH: 1153 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-891-943-3	Ouery Match 100.0%; Score 5956; DB 10; Length 1153; Best Local Similarity 100.0%; Pred. No. 0; Matches 1153; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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901 NVTSENNAPRINKTEPQLELPVKYAVYAVITSHGVSTKYLNFTASENTSRVAQHQYQVSN
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                                               DLTVGAQGHVLLLRSQPVLRVKAIMEFNPRBVARNVFECNDQVVKGKBAGEVRVCLHVQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 1153;
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 1153; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                      Sequence 30. Application US/10144259
| Sequence 30. Application US/10144259
| Publication No. US20030109691A1
| GENERAL INFORMATION:
| APPLICANT: Arnaout, M. Amin
| APPLICANT: Li, Rui
| APPLICANT: Xiong, Jian-Ping
| TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
| TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
| TITLE OF INVENTION: VARIANT US/10/144,259
| CURRENT PILING DATE: 2002-09-04
| FRIOR APPLICATION NUMBER: US 09/758,493
| PRIOR PELLING DATE: 2001-01-11
| PRIOR APPLICATION NUMBER: US 60/221,950
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 0;
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                                                    MMSEGGPPGARPO 1153
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Best Local Similarity 100.
Matches 1153; Conservative
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US-10-144-259-30
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US-10-144-259-30
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LENGTH: 1153
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Sequence 4, Application US/09945265

Factor No. US20020123614A1

Factor No. US20020123614A1

Factor No. US20020123614A1

FAPILICANT: Springer, Timothy A.

APPLICANT: Springer, Timothy A.

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME

FILE REFERENCE: CBN-002CP

CURRENT APPLICATION NUMBER: US 60/229,700

FRIOR PILING DATE: 2001-08-31

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PASLEEQ for Windows Version 4.0

FRIOR PASLED NOS: 4

FOR THE NOS: 4
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                                                                                                                                                                                                                                            Score 5940.5; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                              99.78;
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Best Local Similarity 99.9
Matches 1152; Conservative
                                                                                                                                                                                                       TYPE: PRT
CAGANISM: Homo sapiens
US-09-945-265-4
                                                                                                                                                                                                LENGTH: 1152
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GSLYQCDYSTGSCEPIRLQVPVEAVNWSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
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721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFERNCGNDNICQDDLSITFSFMSLDCLVVG 780
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                                                                  TOGEKFGDPLGYEDVI PEADREGVIRYVI GVGDAFRSEKSRQELAFIASK PPRDHVFQVN
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| Sequence 6, Application US/09902481A
| Publication No. US20030054440A1
| GENERAL INFORMATION:
| APPLICANT: Springer, Timothy
| APPLICANT: Shimao, Julia
| APPLICANT: Shimao, Julia
| APPLICANT: Shimao, Julia
| APPLICANT: Shimao, Stephen
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| FILE REPRENCE: A-70586-1/RFT/RMS/RMK
| CURRENT APPLICATION NUMBER: US/09/902,481A
| CURRENT APPLICATION NUMBER: US 60/216,600
| PRIOR FILING DATE: 2000-07-07
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 6
| LENGTH: 1137
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98.5%; Score 5868; D
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1133; Conservative 3; Mismatches
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ORGANISM: Artificial
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Sequence 4, Application US/09902481A Publication No. US20030054440A1 GENERAL INFORMATION:
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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ORGANISM: Artificial sequence
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OTHER INFORMATION: synthetic
US-09-902-481A-4
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| Publication No. US20030054440A1
| GENERAL INFORMATION:
| APPLICANT: Sprimack, Motomu
| APPLICANT: Shimack, Motomu
| APPLICANT: Mayo, Stephon NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| FILE REPRENCE: A.70586-1/RPT/RMS/RMK
| CURRENT APPLICATION NUMBER: US/09/902,481A
| CURRENT FILING DATE: 2001-07-09
| PRIOR FILING DATE: 2000-07-07
| NUMBER OF SEQ ID NOS: 7
| SECTIVARE: Patentin Version 3.1
| SEQ ID NO 5
| LENGTH: 1137
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ORGANISM: Artificial sequence
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Best Local Similarity 99.3%;
Matches 1129; Conservative
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, OTHER INFORMATION: synthetic
US-09-902-481A-5
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APPLICANT: Springer, Timothy
APPLICANT: Shimacka, Mocomu
APPLICANT: Shimacka, Mocomu
APPLICANT: Shimacka, Motomu
APPLICANT: Shimacka, Motomu
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REPERENCE: A.70586-1/RFT/RMS/RMF
CURRENT FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO 4
LENGTH: 1137
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TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                       Query Match 98.0%;
Best Local Similarity 98.9%;
Matches 1124; Conservative
                                                                                        FEATURE:
COTHER INFORMATION: Synthetic
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FILE REPERRUES: A-70586-1/RFT/RMS/RWK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SSOFTWARE: 1137
                                                                                                                                                                              Score 5839; D
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8; Mismatches
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Sequence 3, Application US/09902481A
Sequence 3, Application No. US20030054440A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
ITILE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
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                                              RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
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                              LLSTVGSYDWAGGVFLYTSKEKSTPINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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US-09-350-259-4
US-09-350-259-4
; Sequence 4, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.;
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Hum;
; TITLE OF INVENTION: No. US20020062008A1el Hum;
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: US/09/350,259
; RARLIER APPLICATION NUMBER: US/09/350,459
; BARLIER APPLICATION NUMBER: 09/193,043
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APPLICANT: Slan pharmaceutical Technology
APPLICANT: Sanch Daniel J.
APPLICANT: Barayden, Daniel J.
APPLICANT: Barayden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Lisa
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REPREMENT: 2002-10-04
NUMBER: US/10/116,275
CURRENT APPLICATION NUMBER: US/10/116,275
NUMBER: OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
SEQ ID NO 204
                                                                                                                                                   RINQTVIWDRPQVIPSENLSSICHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1036
                                                                                                                                                                                                             PFGIOBEPNATIKGNISFDWYIKTSHNHILIVSTABILENDSVFTELPGGGAFVRSQTET 1096
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   GPREFNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840
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Publication No. US20030211476A1
GENERAL INFORMATION:
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                                                                                                68 QCGYSTGACEPIGLQVPPEAVMYSLGISLASTTSPSQLLACGPTVHHECGRUMYLTGLCF
 FSFPGLKSLLVGSNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSL
                                          SIAVCORIQCDIPFFGIOERFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLL
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                                                                               ENNMPRINKTEFOLEL PVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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US-UD-891943.
US-UD-891943.
Publication No. US20030077278A1
GENERAL INFORMATION:
APPLICANT: GAILAIII, Michael W.
APPLICANT: GAILAIII, Michael W.
TITLE OF INVENTION: No. US20030077278A1el Hum
TITLE OF INVENTION: No. US20030077278A1el Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
WUMBER OF SEQ ID NOS: 114
SEQTEMBRE: PATENTIN VET: 2.0
SEQ ID NOS: 114
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                                                                                                                                                                                                    58.4%; Score 3480; DB 9;
larity 61.1%; Pred. No. 1.5e-310;
Conservative 144; Mismatches 294;
EARLIER FILING DATE: 1993-12-23
EARLIER PELING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 4
LENGTH: 1163
                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 697; Conserv
                                                                                                                                                                            US-09-350-259-4
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58.0%; Score 3455; DB 9;
Best Local Similarity 59.9%; Pred, No. 2.9e-308;
Matches 684; Conservative 162; Mismatches 287;
    TITLE OF INVENTION: NO. USEQUECOURTER.
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER PILING DATE: 1999-11-16
EARLIER PILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1993-12-23
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SOFTWARE: PALENTIN VOIL 2.0
No. US20020062008Alel
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CRGANISM: Homo sapiens
US-09-350-259-2
 OF INVENTION:
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                               246 ARRDAIXILIVITDGKKEGDSLDYKDVIPWADAAGIIRYAIGVGLAFQNRNSWKELNDIA
                                                                    SKPPRDHVPQVNNFEALKTIQNQLREKIPAIEGTQTGSSSSPEHEMSQEGFSAAITSNGP
                                                                                   306 SKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETISSSSFELEMAQEGFSAVFTPDGP
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APPLICANT: Gallatin, Michael W.
RAPLICANT: Van der Vieren, Monica
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                                                                                                           244 ARKSAKKILIVITDGQKYKDPLBYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELMTIS 303
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                                                                                             ARKNAPKILVVITDGEKRGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA 304
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Publication No. US2003007727841
GENERAL INFORMATION:
APPLICANT: GALLALIN, Michael W.
APPLICANT: GALLALIN, Michael W.
APPLICANT: GALLALIN, NO. US20030077278Alel Human 2;
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: 09/1943
CURRENT FILING DATE: 2001-06-26
PRIOR PILING DATE: 1998-11-16
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-10-13
PRIOR PILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN NUMBER: 08/943,363
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 S8.0%; Score 3455; DB 10; Similarity 59.9%; Pred. No. 2.9e-308; 34; Conservative 162; Mismatches 287;
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ORGANISM: Homo sapiens
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Best Local Simil
Matches 684; <
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Patent No. 5437958
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 543795881 Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
CORRESPONDENCE ADDRESS: 3 Acker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 6066-6402
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PRADABLE FORM:
MUDIUM TYPE: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION BATA:
FILING DATE:
CLASSIFICATION NUMBER: 35,302
REPERBUSE/DOCKET NUMBER: 27866/31363
TELEFAX: 312-474-6340
TELEFAX: 312-474-6340
TELEFAX: 312-474-6340
TELEFAX: 312-474-6340
TELEFAX: 25-3856
INFORMATION FOR EED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: LISS amino acids
TUPPER. APPLICATION acids
TUPPER. AND ACIDE ACIDES
TELEFAX: 1312-474-0348
TELEFAX: 25-3856
INFORMATION FOR EED ID NO: 3:
LENGTH: LISS amino acids
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US-08-485-618-2

US-08-362-52-2

US-08-665-652-2

US-08-68-293A-2

US-08-193-033-2

US-09-103-03-2

US-09-103-03-2

US-09-688-307A-2

US-08-68-307A-2

US-08-68-307A-2

US-08-68-307A-99

US-08-69-293A-99

US-08-693-303-99

US-09-139-043-99

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US-09-139-043-55

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US-09-350-259-99
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100.0%; Score 5956; Best Local Similarity 100.0%; Pred. No. 0; Matches 1153; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDENHESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-173-497-3
    RESULT 1
US-08-173-497-3
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Sequence 4, Appli
Sequence 6, Appli
                                                                                                  June 7, 2004, 17:07:20 ; Search time 18.6066 Seconds (without alignments) 3199.127 Million cell updates/sec
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5956
1 MALRVILLITALFLCHGFNLD......FYRQYXDMMSBGGPPGAEPQ 1153
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2. \cgn2_6\ptodata/2/iaa/5B_COMB.pep:*

3. \cgn2_6\ptodata/2/iaa/6A_COMB.pep:*

4. \cgn2_6\ptodata/2/iaa/6B_COMB.pep:*

5. \cgn2_6\ptodata/2/iaa/PCTUS_COMB.pep:*

6. \cgn2_6\ptodata/2/iaa/PCTUS_COMB.pep:*

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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S-09-350-259-4
S-08-173-497-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                      181 KKSKTLFSLMQXSBBFRIHFTFKBFQNNPNPRSLVKFITQLLGRTHTATGIRKVVRELFN 240
                                                                                                                                                                             481 HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTFULGDVNGDKLTDVA 540 HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTFULGDVNGDKLTDVA 540
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                  GSLYQCDYSTGSCEPIRLQVEVEANMSLGLSLAATTSPPQLIACGPTVHQTCSENTYVK 120
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                                                                                                                                               241 ITWGARKWAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300
                                                                                                                                                                                                                        361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420
                                                                                                                                                                                                                                                                    421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
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US-08-286-889-3

Sequence 3, Application US/08286889

Sequence 3, Application US/08286889

Sequence 3, Application US/08286889

SETECTA INPORMATION:
APPLICANT: Callatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin 1
TITLE OF INVENTION: No. 5470953el Human 2 Integrin 1
TITLE OF INVENTION: No. 5470953el Human 2 Integrin 1
TITLE OF INVENTION: No. 5470953el Human 2 Integrin 1
TITLE OF INVENTION: South Wacker Drive, 6300 Sear Tower
STATE: 111inois
CONFUTEN: 133 South Wacker Drive, 6300 Sear Tower
STATE: 111inois
COMPUTER: FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Patentin:Release #1.0, Version #1.25
COMPUTER: Patentin:Release #1.0, Version #1.25

CILASSIFICATION: A35

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

FILIEPHONE: 312-474-6300

TELEFRAX: 312-474-6300

TELEFRAX: 313-474-6468

TELEFRX: 25-3856

INFORMATION FOR SER DINO:
TELEFRX: 313-474-6468

TELEFX: 1153 amino acids
TTREE maino acids
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100.0%; Score 5956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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961 LGQRSLPISLVFLVPVRLNQTVINDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLIPGQGAFVRSQTETKVRPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFPKRQYKD 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961 LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
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NTIASKPPRDHVPQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGPSAAIT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840
                                                      SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420
                                                                                                           LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
                                                                                                                              IGAPRYQHIGLVAMFRQNTGMWESNANVKGFQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480
                                                                                                                                                                HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA 540
                                                                                                                                                                             HYXEQTRGGOVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLIDVA 540
                                                                                                                                                                                                                    IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
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2 Integrin Alpha Subunit
                                              Sequence 3, Application US/08485618
Patent No. 572853
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 572853361 Human 2 Integrin
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & 1
RESULT 3
US-08-485-618-3
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120 240 240 180 480 61 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120 180 300 360 420 60 60 1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR GSLYQCDYSTGSCEPIRLQVPVEAVAMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 121 GLCFLFGSNIRQOPQXFPEALRGCPQEDSDIAFLIDGSGSIIPHDPRRWKEFVSTVMEQL 241 ITNGARKNAPKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL NTIASKPPRDHVPQVNNPBALKTIQNQLRBKIPAIEGTQTGSSSSPEHEMSQEGFSAAIT 901 NTIASKPPRDHVPQVNNFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT GLCFLFGSNLRQQPQXFPEALRGCPQEDSD1AFLIDGSGS11PHDFRRMKEFVSTVMBQL ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV LGAPRYQHIGLVAMPRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP MALRVILLTALTLCHGFNLDTENAMTPQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV Gaps ö DB 1; Length 1153; 0; Indels Tower #1.25 ZIP: 60666-6402

ZIP: 60666-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY ABLOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE: US/08/485,618
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE: ABLC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,389
FILING DATE: A-0494
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,389
FILING DATE: A-0494
FILING DATE: A-0494
FILING DATE: A-0494
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr. Joseph A.
REGISTRATION NUMBER: 38,659
REFRENCE/DOCKET NUMBER: 38,659
TELEPHONE: 312-474-630
TELEPHONE: 312-474-630
TELEPHONE: 312-474-630
TELEPHONE: 312-474-630
TELEPHONE: SASO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LUNGCTH: 1153 amino acids Sear 100.0%; Score 5956; 100.0%; Pred. No. 0; ive 0; Mismatches 233 South Wacker Drive, 6300 CITY: Chicago STATE: Illinois COUNTRY: United States ZIP: 60606-6402 Query Match Best Local Similarity 100. Matches 1153; Conservative TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-485-618-3 +-1 121 241 361 61 301 421 ò 셤 ð g ठे 쉼 ð 쉱 ò 음 δ 셤 ठ g Ş

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches
                              CURRENT APPLICATION CALL.

FULING DATE:
CLASSIPICATION 135
FILING DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAWE: WILLIAMS J. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION I
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CURRENT APPLICATION DATA:
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STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3
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1021 VNCSIAVCQRIQCDIPFFGIOBEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF 1080
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Fatent No. 5766850
Fatent No. 576850
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US-08-362-652-3
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241 ITNGARKNAFKILVVITDGEKREDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300
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361 SNGFLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420
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100.0%; Pred. No. 0;
tive 0; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ur., Oseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-6448
TELEPAX: 312-474-6488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Antiber Matches 1153; Conservative
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Best Local Similarity
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                                                                STRDRLRBGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP 720
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            601 DITVGAQGHVLLIRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK 660
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Query Match

100.0%; Score 5956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches
  amino acids
         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
  1153
  LENGTH: 11

TYPE: amir

TYPE: Amir

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TOPOLOGY:

MOLECULE TYPE
US-08-482-293A-3
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GREBRAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Wan der Vieren, Wonica

TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subumit

NUMBER OF SCUENCES: 103

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

TATE: Illinois

CONNTRY: United States

ZIP: 6606-640

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: 1BM PC Compatible

OPERATING SYSTEM: PC-1094/MS.D33

APPLICATION NUMBER: US 08/142,293A

FILING DATE: 21-DEC-1993

PRIOR APPLICATION NUMBER: US 08/32,652

PRIOR APPLICATION NUMBER: US 08/32,652

PRIOR APPLICATION NUMBER: US 08/32,652

FILING DATE: 21-DEC-1994

ATTONEY/ARETY INFORMATION:

MADE: Williams Jr. Joseph A.

REGISTRATION NUMBER: 38,659

REBERRACE/DOCKET UNDOREN: 21-06-00

TELERROWN 1312-414-6300

TELERROWN 1312-414-6300
                                     ORSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLILKA
         LSITFSFMSLDCLVVGGPREFNVTVTVRNDGBDSYRTQVTFFPPLDLSYRKVSTLQNQRS
                                                                                                                                                                                                                                                                                            RESULT 6
US-08-482-293A-3
; Sequence 3, Application US/08482293A
; Patent No. 5831029
                                                                                                                                                                                                                                           MMSEGGPPGARPO 1153
                                                                                                                                                                                                                                                      TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                  GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMGFVSTVMEQL
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                                                1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
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NCIEDPVSPIVIRIMPSLVGTPLSAFGNIRPVIAEDAQRIFTALFPFEXNCGNDNICQDD 780
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                                                                                                                              241 ITWGARKNAFKILVVIITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL
                                                                                                                                                           301 NTIASKPPRDHVPQVNNFBALKTIQNQLREKIFALBGTQTGSSSSFEHEMSQEGFSAAIT
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1 MALRVILLTALTICHGFNILDTENAMTFQENARGFGGSVVQLQGSRVVVGAPQEIVAANQR
                                                                                                  181 KKSKTLFSLAQYSEBFRIHFTFKBFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN
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                                         VNCSIAVCORIOCDIPFFGIOZEFNATLKGNLSPDWYIKTSHNHLLIVSTABILFNDSVF 1080
901 NVTSENNWPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960
                                                  1021 VNCSIAVCQRIQCDIPFFGIQBEFNATLKGNLSPDWYIKTSHWHLLIVSTAEILFNDSVF
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INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1153 anino acids
                                                                                                           MMSEGGPPGARPQ 1153
                                                                                                                                                                                                                                                                                                                                                                                                                              312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-3
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Best Local Similarity
Matches 1153; Conserv
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KKSKTLPSIMOYSESFRIHFTPKRFONNPNPRSLVKPITOLIGRIHTATGIRKVVRELFN 240
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                                                                                RESULT 8

US-09-103-043-3

Sequence 3, Application US/09193043

Patent No. 6251395

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE NO. ELVENTRON: NO. 6251395e1 Human 2
FILLE REFERENCE: 27866/35004

CURRENT PILIOR DATE: 1998-11-16

EARLIER PELLING DATE: 1993-12-23

EARLIER PELLING DATE: 1993-12-23

EARLIER PILING DATE: 1994-08-05

EARLIER PILING DATE: 1994-08-05

EARLIER PILING DATE: 1994-12-21

RARLIER FILING DATE: 1994-08-05

EARLIER PILING DATE: 1994-08-05

EARLIER FILING DATE: 1994-08-05

EARLIER FILING DATE: 1994-08-05

EARLIER PILING DATE: 1997-10-03

NOWERR OF SED ID NOS: 114

SEQ IN NO
                                                 1141 MMSEGGPPGAEPQ 1153
                                     1141 MMSEGGPPGAEPO 1153
                                                                                                                                                                                                                                                                                              LENGTH: 1153
TYPE: PRT
GRANISM: Homo sapiens
US-09-193-043-3
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1021 us-09-902-481b-1.raı 8 8 1153; Length DB 4; 05:59:06 2004 ; SEQ ID NO 3 ; LENGTH: 1153 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-688-307A-3 φ

NCIEDPUSPIVLRINFSLUGFPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD 780 840 NVTSENUMPRINKTEPQLELPVKYAVYMVTSHGVSTKYLMPTASENTSRVMQHQYQVSN 960 241 ITNGARKONAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRGEL 300 241 ITNGARKONAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300 660 99 720 720 840 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQL 180 240 240 9 9 DETVGAQGHVLILIRSQPVLRVKAIMBENPREVARNVFBCNDQVVKGKEAGEVRVCLHVQK Gaps . 0 Indels ö Query Match
100.0%; Score 5956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 601 661 721 781 901 721 841 841 301 601 661 781 61 61 121 121 181 181 301 361 361 8 8 g 8 8 8 8 & 8 õ Š 台 원 ઠે

1080 RESULT 10

US-09-150-29-3

Sequence 3, Application US/09350259

Patent No. 6620915

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE REFERENCE: 27866/35004

CURRENT APPLICATION NUMBER: US/09/350, 259

CURRENT FILING DATE: 1999-07-08

RARLIER FILING DATE: 1998-11-16

RARLIER FILING DATE: 1998-11-16

RARLIER FILING DATE: 1994-08-05

RARLIER FILING DATE: 1994-08-05

RARLIER FILING DATE: 1994-08-05

RARLIER FILING DATE: 1994-12-21

RARLIER FILING DATE: 1994-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTY OF THE NUMBER: 08/362, 652

RARLIER FILING DATE: 1994-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTY OF SEQ ID NOS: 114

CENCTH: 1153

TTPE: PRT

TTPE: PRT MACEGGPPGAEPO 1153 1141 MMSEGGPPGAEPO 1153 1141 1081 1001 1021 के क्षे के 음 중 음

Gaps ö 1153; Length Indels ö DB 4; Query Match
100.0%; Score 5956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches

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61 GSLYQCDYSTGSCEPIRLQVPVEAVMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVX 120
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361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDWNDAYLGYAAAIILENRVQSLV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GLCFLFGSNLRQQPQKPPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 180
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99.5%; Score 5925.5; DB 2; Length 1152;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1150; Conservative 0; Mismatches 2; Indels 1;
COUNTRY: US

IIP: 02110-2804
COMPUTER: EADABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 09/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: 07/512,573
FILING DATE: 28-JUN-1998
ATTORNEY/AGENT INPORMATION:
NAME: Freeman, John W
REGISTRATION NUMBER: 29,066
REFERENCE/DOCTEST NUMBER: 00786/068003
TELERPHONE: 617/542-5070
TELERPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 61/542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
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                              SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420
                                            SMGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420
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Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: ATMAGULA AMAIN
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: BOSCON
STATE: MA
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61 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KKSKTLFSLMQYSEBPRIHFTFKEPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ITNGARKOAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRVVIGVGDAFRSEKSRQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MALRVLALTALTALTALCHGFNLDTERAMTFQENARGFGGSVVQLQGSRVVVGAPQEIVAANQR
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 PILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
RECISTATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-806
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152
                                                                                                                                                                                                                                     99.5%; Score 5925.5;
99.7%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                               Matches 1150; Conservative
                                                                                                                                                                  TYPE: amino acid
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STRANDEDNESS:
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TOPOLOGY: linear
PCT-US96-01314-43
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US-08-476-062A-44
i Sequence 44. Application US/08476062A
; Sequence 44. Application US/08476062A
; Patent NO. 5877275
; GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONPROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
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                    LSITFSFMSLDCLVVGGPRESNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                                                                             QRSWRLACBSASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKA
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5424399-2
; PATENT NO. 5424399
; PATENT NO. 5424399
; TILLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/78,871
; ILING DATE: 16-UN-1993
; PRIOR APPLICATION DATA;
APPLICATION NUMBER: 539,842
; APPLICATION NUMBER: 539,842
; APPLICATION NUMBER: 539,842
; APPLICATION NUMBER: 212,573
; PILING DATE: 18-UN-1980
; APPLICATION NUMBER: 212,573
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.7%;
Matches 1150; Conservative
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                                                 GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
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PCT-US96-01314-44
; Sequence 44, Application PC/TUS9601314
GENERAL INPORMATION:
    APPLICANT: M. Amin Arnacut
    TITLE OF INVENTION: METHODS POR IDENTIFYING INTEGRIN
    TITLE OF INVENTION: METHODS POR IDENTIFYING INTEGRIN
    TITLE OF INVENTION: METHODS POR IDENTIFYING INTEGRIN
    TITLE OF SEQUENCES: 78
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: 78 FABARIAN & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STREET: 225 Franklin Street
    COUNTRY: U.S.A.
    ZIP: Boston
    STREET: 220 Franklin Street
    COUNTRY: U.S.A.
    ZIP: ADDRESSEE: Nanklin Street
    CONPUTER: Boston
    SOFTWARE: WordPerfect (Version 5.0)
    COMPUTER: IBM PS/2 Model 502 or 555X
    OPERATING SYSTEM: MS-DOS (Version 5.0)
    CURRENT APPLICATION DATA:
    APPLICATION UNMBER: PCT/US96/01314
    FILING DATE: 30-JAN-96
    PRIOR APPLICATION DATA:
    APPLICATION
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            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: DISKETE COMPUTER: EMACOWALID!
COMPUTER: REALESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-UNA-1995
RILING DATE: 12-WAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 18-JUNA-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 07/212,573
FILING DATE: 18-JUN-1981
REGISTRATION NUMBER: 29,066
REFERRANCE/DOCKER NUMBER: 00786/068003
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
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amino acid
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                                                                                                                                                                      Length 1163;
                                                                                                                                                                   58.8%; Score 3503; DB 5; Length 1 llarity 61.3%; Pred. No. 3.8e-287; Conservative 138; Mismatches 297; Indels
                               00786/267001
     NAME: JOHN W. Preeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKER UNMER: 0078
RELECOMMUNICATION: TELEPOWE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                     TOPOLOGY: linear
PCT-US96-01314-44
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 700; Conserv
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                                                                                                                        1083 PGQEAFWRAQTTTVLEKYKVHNPTPLIVGSSIGGLLLLALITAVLYKVGFPKRQYKENMB
                                                                     ENNMPRTNKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTAS - ENTSRVMQHQYQVSNLGQ
                                                                                                                                                  SIAVCORIQCDIPPPGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTARILFNDSVFTLL
                                                                                                                                                                                           PCOCAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
                                                                                                                                                               845 HLTCDSAPVG--SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTAANVSS
                               845 RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS
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Search completed: June 7, 2004, 17:19:16 Job time: 23.6066 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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June 7, 2004, 17:05:16; Search time 14.559 Seconds (without alignments) 7512.163 Million cell updates/sec protein search, using sw model OM protein -

Run on:

US-09-902-481B-3 5879 1 FNLDTENAMTFQENARGPGQ......FKRQYKDMMSEGGPPGABPQ 1137 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283366 segs, 96191526 residues Searched:

0.5

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cell surface glyco	ocyte su		9	re fr	integrin alpha-E c	integrin alpha-1 c	먑	otein h		integrin alpha-1 c	:e-Peyer'	lpha-4	alpha-	integrin alpha cha	nteg	aurface	pha s	alpha	integrin alpha-V c	alpha-	alp	tin recep	ntegrin alp	alpha-5	alpha	alpha-6	alpha-8	position-specific
SUMMARIES	ΩI	RWHU18	800551	RWHU1C	803308	156126	A53213	A45226	145914	S44142	A33998	A35854	A41131	506046	158409	T31437	JC7294	A35761	155534	S44250	A36108	T10050	A38457	A27079	B36429	A27421	A40021	A41543	651	A29637
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S40311	A34269	JC5950	161186	A60163	B30892	S38783	S44824	S60571	\$28277	T09403	T09433	136916	T18523	136917	A55348
8	N	N	7	N	7	N	N	7	7	7	7	C	N	~	7
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496.5	496	491	490	487.5	486	470	466	458.5	444.5	418	413.5	391	309	299	279.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.0

ALIGNMENTS

NAILernate daycoprotein CD11b precursor [validated] - human
NyAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein }
NyAlternate names: complement receptor type 3 alpha chain; leukocyte alpham chain
E;beries: Homo sapiens (man)
C;bate: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 31-Dec-2000
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A,L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, 4)

A; Reference number: A31108; MUID:88315033; PMID:2457584

Ajaccession: A31108
Ajaccession: A31106
Ajacce

A; Molecule type: mRNA A; Residues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> A; Cross-references: GB:MIGN44 A; Cross-references: GB:MIGN644 A; Cross-references: GB:MIGN644 A; Title: CDNA sequence for the alphaM subunit of the human neutrophil adherence recept: A; Accession: A32218; MUID:89098893; PMID:2563162 A; Accession: A32218 A; Michaelt type: mRNA A; Residues: 9-1153 <AIIC> A; Cross-references: GB:J04145; NID:9189068; PIDN:AAAS9903.1; PID:9386975

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chain reveals homology with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     917 OLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
                                    377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                                                                361 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                                                                              421 ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVT.IGAPHYYEQTRGGQVSVCPL
                                                                                                                                                                                                                                                                                                                                      481 PRGQRARWQCDAVLYGBQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                                                497 PRGORARWOCDAVLYGEQGOPWGRFGAALTVIGDVNGDKLTDVAIGAPGBEDNRGAVYLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 YDLALDSGRPHSRAVENKTKNSTRRQTQVLGLTQTCSTLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPRBENVTVTVRNDGEDSYRIQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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A;Molecule type: DNA
A;Redidues: 1-1153 <-Pyr>
A;Cesidues: 1-1153 <-Pyr>
A;Cesidues: 1-1153 <-Pyr>
A;Cesidues: 1-1153 <-Pyr>
A;Crosa-references: EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A;Note: the authors translated the codon CAC for residue 569 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mac-1 alpha c
PMID:3044779
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A;Molecule type: DNA

A;Note: part of this sequence was confirmed by protein sequencing
R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in a during evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-9 <RES>
A;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forws a heterodimer with this chain to form Mac-1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 17-31 <PIES-
A; Experimental source: granulocytes
R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A; Title: Characterization of the myeloid-specific CD11b promoter.
A; Reference number: 152567; MUID:92144986; PMID:1346576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.3%; Score 5839;
98.9%; Pred. No. 0;
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                                                                                                                                                                       A; Accession: A46526
A; Status: not compar
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R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5649, 1986
A;Ittle: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: 159078
A;Reference number: 159078
MUID:86287312; PMID:342940
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 11.44 - RES>
A;Genetics:
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A;Genetics: A;Genetics: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
C;Genetics:
A;Genetics: Binal sequence #status predicted <SIG>
C;Keywords: cell adhesion; glycoprotein, transmembrane protein
F;1.16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: leukcoyte surface glycoprotein Mac-1 alpha chain #status experimental F;148-318/Domain: von Willebrand factor type A repeat homology <WMA2>
F;1106-1129/Domain: bransmembrane #status predicted <TWM>
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Whill surface glycoprotein CD12 precursor - human

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Gaps ç, Length 1163; Indels 58.8%; Score 3456; DB I; llarity 60.6%; Pred. No. 1.2e-233; Conservative 143; Mismatches 296; Similarity 684; Query Match Best Local S Matches 684

PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF 180 240 CHPTFEEFRATSNPLSLLASVHQLQGFTYTATAIQNVVHRLFHASYGARRDATKILIVI 257 61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 TOGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSROBLNTVASKPPRDHVFQAN 300 79 RIHFTPKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL |||||||| FNLDTEBLTAPRUDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLXQCGYSTGACBPI 1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQRIVAANQRGSLYQCDYSTGSCEPI 121 181 198

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PPFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE 1079

1080 TKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE Š

1095 TVLEKYKVHNPTPLIVGSSIGGLLLLALITAVLYKVGPPKROYKEMMBE 셤

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tch 26.1%; Score 1532.5; DB 2; Length 1170; sal Similarity 34.2%; Pred. No. 9.7e-99; 401; Conservative 209; Mismatches 463; Indels 101; Gaps Query Match Best Local S Matches 401

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28 26 YNLDVRGARSFSPPRAGRHFGYRVLQV-GNGVIVGAPGE---GNSTGSLYQCQSGTGHCL 1 FNLDTENAMIFQ--BNARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSIGSCE

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PIRLOVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLR---82 PVTLR-GSNYTSKYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSGLCYLFRQNLQGPM 29 ò d

141 LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAV 196 116 -QQPQKPPBALRGCPQBDSDIAFLIDGSGSIIPHDFRRWKELVSTIMEQLKKSKTLFSEM ò

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           GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTR
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QYSEBPRIHFTFKEFQNNPNPRSLIKPITQLLGRIHTATGLRKVVRELFNITMGARKNAP
                                      KILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRD
                                                                              HVFQANNFEALKTVQNQLREKIFA:EGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVG
                                                                                                                                        AKDWAGGFLDLKADLQDDTPIGNEPLTPEVRAGYLGYTVTWLPSRQKTSLLASGAPRYQH
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156126 Lymphocyte fuction-associated molecule-1-alpha - mouse

RESULT 5

A repeat homo molecule-1 alpha-subunit 119 309 356 414 429 472 489 532 545 592 603 767 651 661 S O 7.9 Species: Mus musculus (house mouse) Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999 60 IRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQ : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : DWAGGVF-LYTSKEKSTPINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQHIG 533 NRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQG EGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV SPINVSLNPSLLEBEGTPRDQKGRAMQPILRPSIHTV-TKEIPFEKNCGEDKKCEANLTL C;Species: Mus musculus (house mouse)
C;Date: 26-Uul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1996
C;Accession: 156126
B;Kaufmann, Y.; Tseng, E.; Springer, T.A.
J. Immunol. 147, 359-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 al A;Reference number: 156126; MUID:91268576; PMID:2051027
A;Accession: 156126
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1163 <RES>
A;Residues: 1-1163 <RES>
A;Cross-references: GB:M60778; NID:9198785; PIDN:AAA39426.1; PID:9198786
C;Genetics:
A;Genetics: A;Genetics: A;Shomain: von Willebrand factor type A repeat homology <VWAl> type KPPEALRGCPQEDSDIAPLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEE FRIHFTFKEF-QNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILF LLTDGEKF--GDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHV POANNFRALKTVONQLREKIPALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSY 415 LVAMFR--QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRG GOVSVCPLPRGORARWOCDAVLYGEOGOPWGRFGAALTVLGDVNGDKLTDVALGAPGEED 593 HVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAG-BVRVCLHVQKSTRDRLR SPIVLRLNFSLV---GTPLSAFGN-LRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSI FINIDITENAMI FORNA - RGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEP Gaps PID:9198786 Match 25.8%; Score 1516.5; DB 2; Length 1163; Local Similarity 33.9%; Pred. No. 1.3e-97; Loservative 216; Mismatches 466; Indels 89; Н 80 24 180 259 120 297 357 370 490 661 239 473 652 721 Query Mat Best Loca Matches 셤 6 6 6 6 6 6 6 6 6 ઠે 셤 8 8 8 유 상 R ద ò g 8 6 8

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18.5%; Score 1085.5; DB 2; Length 1151;
Best Local Similarity 27.6%; Pred. No. 2.1e-67;
Matches 342; Conservative 209; Mismatches 488; Indels 201;
A;Accession: A45226
A;Status: preliminary, not compared with conceptual translation A;Status: preliminary
A;Macule type: man,A
A;Residues: 1-1151 <BRI>A;Residues: 1-1151 <BRI>A;Residues: 1-1151 <BRI>A;Reperimental source: hepatoblastoma cell line HepG2
A;Mote: sequence extracted from NCBI backbone (NCBIP:124326)
P;142-317/Domain: von Willebrand factor type A repeat homology.
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                                                                         108 FLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLK-- 165
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Cjspecies: Bos primigenius taurus (cattle)
Cjspecies: Bos primigenius taurus (cattle)
Cjaccession: 145914
Rjkamata, T.: Paran, W.; Pakada, Y.
Rjkamata, T.: Paran, W.; Pakada, Y.
Ajtle: Identification of putative ligand binding sites within the I-domain Ajtlesenon: 14594
Ajtle: Identification of putative ligand binding sites within the I-domain Ajtlescession: 145914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 KSKTLPSLMQYSEEFRIHFTFKEFQNNPNPRSLIKPITQLL----GRTHTATGLRKVVRE
                                                                                                                                                                                                                                                                                           QLELPVKYAVYMVTSHGVSTKYLNPTASENTSRVMQHQYQVSN-----LGQRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LPISLVF------LVPVRLNQTVIWDRPQVTFSENLSSTCHTKG------R
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*Kseidues: 1-1170 «XMA»
A; Cross-references: GB:L25886; NID:g439695; PIDN:AAB59255.1; PID:g439696
F;161-336/Domain: von Willebrand factor type A repeat homology «VMA2»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.2%; Score 1071; DB 2; Length 1170;
Best Local Similarity 27.5%; Pred. No. 2.2e-66;
Matches 334; Conservative 218; Mismatches 495; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPSHSDFLABLRKAPVVNCSIAVCQRIQCDIPFFGIQE------
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Length 1178;

439 AAIILRRRVOSLVILOAPRYQHIGLVAMPRQNTGAMBESNANVKGTOGGARGEGASCASO VASISTGANSVHFVAGARRANTGQILIZSVNEGGNTVUGGGRADGIGSTGSTGANGARRANTGGILIZSVNEGGNTVUGGGRADGIGSTGANGARGANTGGANGARGANTGGILIZSVNEGGNTVUGGGRADGIGSTGANGARGANTGGANGARGANTGGANGARGANTGGANGARGANTGGANGANGANTGGANGANGANGANGANGANGANGANGANGANGANGANGAN	AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWBSNANVKGTQLGAYFGASL 445	CSVDVDSNASTDLVLIGAPHYYEQTRGGQVSVCPLPRQRARMQCDAVLYGEQQQPWG 503		707 733	156	DD REVLAEDAQRIFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTV 789	848	864	SSINHPIPPENSEVTRNITPDVDSKASLGNKLLLKANVTSENNMPRINKTBFQLELPVKY 908	923	SLPISLVFLV 958	HSFEDIGPKFIFSIKVTTGSVPVSMA 976		1030	LEKAPVANCSIAVCQRIQCDIPPEGIQEBFNATEKGNLSPDWYIKTSHNHLLIVSTAEI- 1057	PRHIKELNCRIASCSNIMCWIRDLQVKGEYFINVSTRIWNGTFAASTFQTVQLTAAAEID 1090	LFNDSVFTLLPGQGAFVRSQTETKVEPFE-VPNPLPLIVGSSVGGLLLLALITA 1110	LILIALVA 1140	qa —	ζ
													PVRL	1				TYNPOIYVIBENTVTIP	ALYKLGFFKROYKDM	: : : ILWKLGFFKRKYEKM

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L.; Latze
RABOULT 9
784142
VLA-2 protein homolog - mouse
C.Species: Mis musculus (house mouse)
C.Species: Mis musculus (house mouse)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Sep-2003
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Sep-2003
C.Accession: 844142
R.Edelnan, J.M.; Chan, B.M.; Uniyal, S.; Omodera, H.; Wang, D.Z.; Damjanovich, L.; L. A.Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but A.Description: S44142
A.Decession: 844142
A.Accession: 844142
A.Accession: 848142
A.Residues: preliminary
A.Molecule type: mRNA
A.Residues: 1-1178
A.Residues: 1-1178
A.Residues: 1-1178
A.Residues: 1-1178
A.Residues: L. Accession: Von Willebrand factor type A repeat homology vWR2>
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45 437 505 55 GSCEPIRIQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107 | 147 ----SDVSPDPQFLTSFSPAVQACPSL-VDVVVVCDESNSIYP--WEAVKNFLVKFVTGL 199 :: :|: :|| | : || | : || 319 TKNLIKEIKATASTERYFINVADEAALLEKAGTLGEQIPSIEGTVQG-GDNFQMEMAQ 377 447 494 551 564 610 999 PLFGSNLRQOPQ---KFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQL 164 SEKSRQELNTVASKPPRDHVFQANNPEALKTVQNQLREKIFAIEGTQTGSSSSFEHEMSQ 336 RGFSA--AITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 623 619 717 737 768 788 823 847 871 905 928 984 86 54 222 LFNITNGARKNAFKILFLLTDGEKFGDPLGYEDVIPELDREGVIRY---VLGF--GDAFR VDVDSNGSTDLVLIGAPHYYEOTR - - GGOVSVCPLPRGORARWOCDAVLYGEQGPWGRF KNSTRRQTQVLGLTQTCET -- LXLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVL 165 K--KSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLIKPITQLLG-RTHTATGLRKWYRE GAALTVLGDVNGDXLTDVAIGAPGBEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR-611 HLQFFGRSLDGYGDLMGDSITDVS1GALGQVIQLWSQSIADVAIBALFTP------SERFLQKOMYVVNEVQKCSEHHISIQKPS---DVVNPLDLRVDISLENPGTS-----PAL VIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKST SCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTE--PQLELP VKYAVYMVVISHGVSTXYLNFTASENTSRVMQHQYQVSNLGQR-----SLPISLV Gaps 1 FNLDTENAMTFQ-ENARGFGQSVVQL---QGSRVVVGAPQBIVAANQRGSLYQC--DYST 392 AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGTQIGAYPGASLCS 565 -LQYPGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFEC NDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFNET AEDAQRIPTALFPFEKNCGNDNICQDDISI-----TPSFMSLDCLVVGGPREFNVT Indels 188; / Match 18:0%; Score 1057; DB 2; I Local Similarity 27.8%; Pred. No. 2.2e-65; nes 341; Conservative 209; Mismatches 487; 277 337 448 624 680 872 206 169 789 848 8 6 8 6 8 6 σ

108 FLEGSNIRQOPOKFPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMBOLK 165 150 SDISPDF-QLSASFSPATQPCPSL-IDVVVVCDESNSIYFWDAVKNPLEKFVQGLDIG 205 166 KSKTLPSLMQYSEBFRIHFTFKEPQNNPNPRSLIKPITQLLG-RITHTATGLRKVVRELFN 224 16 KSKTLPSLMQYSEBFRIHFTFKEPQNNPNPRSLIKPITQLLG-RITHTATGLRKVVRELFN 224 16 KSKTLPSLMQYSEBFRIHFTFKEPQNNPNPRSLIKPITQLLG-RITHTATGLRKVVRELFN 224 206 FKTQVGLLQYANNPRVVFNLATYTKREMIVATSQTSQYGGDLTNTTGALQYARKYAYS 265 217 ITNGARKNAFKILIDGEKFGDPLGYBENDFELDREGVIRYUGF-GDAFRSEK 279 226 AASGGRRSATKVWVVTDGESH-DGSMLKAVIDQCNHDNILRFGIAVLGYLNRNALDTKN 324 237 STQELNTVASKPPRDHVPQANNFEALKTVQNQLREKIPAIEGTGTGSSSSFBEHEMSQEGF 339 238 LIKEIKAIASIPTERYFRNSDEAALLEKAGTLGBQIFSIBGTVQG-GDNFQNEMSQVGF 383	SADITSMOP-LIGITEMTETAVADEAGLILEANGTIEGIAGO SENTICADA SEN	LEIVSTARI-LFNDSVPTLLPGQGAFVRSQTBTKVBFPEVPNPLPLIVGSSVG ::: : : : : : : : : : : : :
8 6 8 6 8 6		8 8
985 ELV	Figure 10 All Cerrate names: Chain precursor - human All Cerrate names: CL099b; platelet glycoprotein GPIs; VIA-2/collagen receptor alpha-2 Bection: 10-Mar-1899 #sequence revision 18-Sep-1992 #text_change 15-Sep-2003 Takkda Xi; Menler, ME. Takerence number: A33999; MUID:89308879; PMID:2545729 Molecule type: mRNA Accession: A33998 Accession: A33999; MUID:89308879; PMID:2545729 Molecule type: mRNA Accession: B56739; MUID:92061944; PMID:2545729 Molecule type: mRNA Accession: B56739; MUID:92061944; PMID:195540 Molecule type: mRNA Accession: B56739; MUID:92061944; PMID:195540 Molecule type: mrNA Mole	Db 30 YNVGLPEAKIFSGPSSEQFGYAVQQFINPKGNWLLVGSFWSGFPENRMGDVYKCPVDLST 89 Qy 55 GSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107

Colore 20 cot 2	AND ORLETTALEPERKNOCHNDINCODDISTIPSTWEID 7: [DOALPHSVHEHIPPAKDCCHNERCISDLTLANSTTEKS 8: [DOALPHSVHEHIPPAKDCCHNERCISDLTLANSTTEKS 8: [SI
613 Qy 53 613 Db 101 677 Gy 96	
670 Qy 96	TCSENTYKGALCHGSNLKQQPQKFFKALKGCPQEDSDIAFILLGGGGIIFALFANGAL

දු පු	156 LVSTIMBQLXKSKTLFSLMQYSEBFRIHFTFKBFQNNPNPRSLIKPITQLLGRTHTATGL 215	RESULT 13 S06046 integrin alpha-4
ò	DVIPELDREGVIRYVLGPGDAF 27	N;Alternate name: C;Species: Homo
qq	:	C;Date: 01-Dec-1: C;Accession: S06: P:Takada v v v1
ò	276 RSEKSRQELMTVASKPPRDHVFQANNFBALKTVQNQLREKIFAIEGTQTGSSSSFBHEMS 335	EMBO J. 8, 1361-
ф	203 ASC 205	A;Reference numb
8 7	QEGPSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAVLGYA	A; Molecule type: A; Residues: 1-10
ga .	QAGISSFYTQDLIVMGAPGSSYWTGTVFVYNITTNQYKAFVDRQNQVKFGSYLGYSVG	A, Cross-reference R, Rosen, G.D.; B.
& 6	392 AAIILRNRVQSLVIGAPRYQHIGLVAMPRQNTGWWBSNANVKGTQIGARFGASLCS 447 [Proc. Natl. Acad A;Title: Charact:
ò	VDVDSNGSTDLVL1GAPHYYEOTRGGOVSVCPL PRGORA-RWOCDAVI-VGEDGOODWGBEG	A; Accession: A39:
; d		A;Residues: 1-93 A;Cross-reference
È	507 AALIVIGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQ 566	R; Takada, Y.; St. Proc. Natl. Acad
qq	:: ::	A;Reference numb
δ	567 YFGQSLSGGQDLTMDGLVDLTVGAQGHVILLRSQPVLRVKAIMERNPREVARNVFBCN 624	A; Accession: D28 A; Molecule type:
qq	436 MFGQSISGQIDADNNGYVDVAVGAFQSDSAVILRTRPVVIVEASLS-HPESVNRTKRDCT 494	A; Residues: 40-5 C; Genetics:
È	625 DQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNET 679	A; Cross-reference
д	ILTLCFSYKGKEVÞGYIVLFY	A; Map position: C; Superfamily: i
È	680 KNSTRRÇTQVLGLTQTCETLKLQLPNCIEDPVSPIVLALNFSLVGTPLSAFGNLR 734	C;Keywords: cell F;1-39/Domain: B;
Q	548 SDVITGSIRVSSSGEKCRTHQAFMRKDVRDILTPIHVEATYHLGHHVITKRNTEBFPPLQ 607	Danoay Rectange
È	735 PVLAEDAQR-LFTALFPFEKNCGNDXICQDDLSITFSFWSLDCLVVGGPREFNV 787	Query March Best Local Sim: Matches 293:
eg G	608 PILQQKKBKDVIRKMINFARFCAYEN-CSADLQVSAKVGFLKPYENKTYLAVGSMKTIML 666	100
à	788 TVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKST 847	
qq	667 NVSLFNAGDDAYFTTLNVQLPTGLYFIKILDLEEKQINCEVTESGGIVK-L 716	יי יי
ઠે	848 SCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLELP 905	53
Dio		100
Š	906 VKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFL 957	110
ďű	777 LRYEVMLTVHGLVNPTSFVYGSSEENEPETCMAEKINLTFHVINTGISMAPNVSVKIM 834	134
ζ	958 VPVRLINGTVINDRPQVIFSENLSSTCHTKERLPSHSDFLAELR 1000	170
qq	835 VPNSFLPQDDKLFNVCLDVQTTTGQCHFKHYGRECTFAQQKGIAGTLTDIVKFLSKTD 891	157
ò	1001 KAPVVNÇSIAVÇQRIQÇDIPPFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTABIL 1058	230
QQ	892 KR-LLYCMKADQHCLDFLCNFGKMESGKRASVHIQLEGRPSIL 933	161
ά	1059 FNDSVPTLLPGQGAFVRSQTETKVEPFEVPNP 1090	
qa	934 EMDETSSLKFBIKATAFPEPHPKVIBLNKDENVAHVFLEGLHHQRPKRHF 983	204
ò	1091 -LPLIVGSSVGGLLLEALITAALYKIGFFKRQYKDMMSB 1128	Db 212 YE
ପୁପ	984 TIIITISELLGLIVLLISCVMWKAGFFKRQYKSILQB 1022	Qy 398 NR

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nces: GB:M62841
Strominger, J.L.; Hemler, M.E.
ad. Sci. U.S.A. 84, 3239-3243, 1987
ad. Sci. U.S.A. 84, 3239-6243, 1987
ary late antigen family of heterodimers is part of a superfamily of molect
ber: A94151; MUID:87204112; PMID:3033641
                                                                                                                                                           imary structure of the alpha(4) subunit of VLA-4: homology to other inteber: $06046; WUID:89356603; PWID:2788572
6046
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I adhesion, cytoskeleton, duplication, glycoprotein, heterodimer, transm
signal sequence #status predicted <SIG>
ct: integrin VLA-4 alpha-4 chain #status predicted <MAT>
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4 chain precursor - human
es: COD401, very late antigen-4 alpha chain; VLA-4 alpha chain
sapiens (man)
1989 #sequence_revision 01-Dec-1989 #text_change 24-Sep-1999
6046; A39355; D28018
Lices, M.J.; Crouse, C.; Hemler, M.E.
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.larity 23.6%; Pred. No. 2.2e-36;
Conservative 170; Mismatches 408; Indels 368; Gaps
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50,'E',52-53 <TA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                   YA--AAIILRNRVQSLVLGAPRYQHIGLVAMFR--QNTGMWESNANVKGTQIGAYFGASL
A,Title: Sequence and tissue distribution of the integrin alpha9 subunit, A,Reference number: A49459; MUID:94064789; PMID:8245132
A,Accession: A49459
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 30-1035 < PAL>
A,Cross-references: GB:L24158
A,Cross-references: GB:L24158
C,Superfemally: integrin alpha-4 chain
C,Keywords: glycoprotein; metal binding; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <51G>
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                                                                                                                                                                                                                                               . Match 10.7%; Score 630; DB 2; L. Local Similarity 26.5%; Pred. No. 1.5e-35; les 237; Conservative 160; Mismatches 332;
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: 158409; A49459
R;Hibi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; 7
Oncogene 9, 611-619, 1394
A;Reference number: 158409; MUID:94119603; PMID:8290272
A;Accession: 158409
A;Attle: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in s
A;Reference number: 158409; MUID:94119603; PMID:8290272
A;Accession: 158409
A;Attle: Aberrant upregulated from GB/EMBL/DDBJ
A;Attle: Tellinary; translated from GB/EMBL/DDBJ
A;Accessidues: 1-1035 cRES-
A;Accessidues: 1-1035 cRES-
A;Accessidues: L:; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
Cell Biol: 123, 1289-1297, 1993
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                                                                                                                                                                                   SIQVSSREANCRIHQAFMRKOVRDILITPIQIEAAYHLGPHVISKRSTEEFPPLQPILQQK 612
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                                                                     GSTDLVLIGAPHYYEOTRGGOVSVCPLPRGORARWOC-DAVLYGEOGOPWGRFGAALTVL 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINH 853
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Tal437
integral alpha chain SU2 - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: Tal437
R;Hertzler, P.L; McClay, D.R.
Submitted to the BMBL Data Library, May 1998
A;Description: Alpha SU2, a sea urchin integrin which binds laminin.
A;Reference number: 221035
A;Accession: T31437
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1041 <HER>A;Cross-references: EMBL:AF067658; NID:g3220240; PID:g3220241; PIDN:AAC23572.1
A;Eurction: binds laminin
C;Superimental source: developmental stage embryo
C;Function: binds laminin
C;Superfamily: integrin alpha-2b chain
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Best Local Similarity 24.8%; Pred. No. 1.9e-34;
Matches 236; Conservative 155; Mismatches 314; Indels 245; Gaps
963 TVVFEALHNLEPRGYVVGWIIAISLLVGILIFLLLAVLLWKMGFFRRRYKEII 1015
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June 7, 2004, 16:55:38; Search time 9.97194 Seconds (without alignments) 5937.039 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

US-09-902-481B-3 5879 1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGFPGAEFQ 1137

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RA MEDLINE-98226734; PubMed=9560195;

RA MEDLINE-98226734; PubMed=9560195;

RA MEDLINE-18 ANDICAT TA.;

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MEDLINE=95171458; PubMed=7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
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MEDLINE=96363671; PubMed=8747460;
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"Two conformations of the integrin A-domain (I-domain): a pathway for
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MEDLINE=9826255; PubMed=9687375;
Baldwin E.T. Sarver R.W. Bernard G.L. Jr., Curry K.A.,
Pairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
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DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A WAPA DOMAIN. INTEGRINS WITH I-DOMAINS OF TEASED CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains I WWPA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
DATABASE: NAME-EROW; NOTE-CD guide CD1lb entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd1lb.htm".

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PROSITE; PS00342; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
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GO; GO:0004895; F:cell adhesion receptor activity; TAS.
GO; GO:0004895; F:cell adhesion, TAS.
InterPro; IPR001413; Integrin_alpha.
InterPro; IPR002035; WWP.A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF01839; Integrin_A; 1.
PRINTS; FR0185; INTEGRINA.
PRINTS; FR0185; INTEGRINA.
PRINTS; FR0185; INTEGRINA.
SWART; SM0191; Int. alpha; 4.
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EXTRACELEULAR (POTENTIAL)
POTENTIAL.
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                                                                                 EMBL; M18044; AAA59544.1; EMBL; M18044; AAA5949.1; EMBL; J04145; AAA5993.1; EMBL; S22227; AAB24821.1; EMBL; S22152; AAB24821.1; J0INED. EMBL; S22153; AAB24821.1; J0INED. EMBL; S22155; AAB24821.1; J0INED. EMBL; S22157; AAB24821.1; J0INED. EMBL; S22157; AAB24821.1; J0INED. EMBL; S22157; AAB24821.1; J0INED. EMBL; S22167; AAB24821.1; J0INED. EMBL; S22177; AAB24821.1; J0INED.
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AAB24821.1;
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EMEL, S52216; AA524821
EMEL, S52216; AA54824821
EMEL, S52220; AA524821
EMEL, S52221; AA624821
EMEL, S52221; AA624821
EMEL, S52222; AA624821
EMEL, S52226; AA624821
EMEL, M76724; AAA58410
EMEL, M76724; AAA58410
EMEL, M76724; AAA5940
EMEL, M84477; AAA51960
PDB, 1BHO, 1B-NOV-98.
PDB, 1BHO, 1B-NOV-98.
PDB, 11DN, 25-NOV-98.
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EMBL;
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1020 1035 300 480 99 720 795 960 120 180 196 240 256 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELATIASKPPRDHVFQVN 316 360 376 420 436 496 540 555 600 615 675 735 780 840 855 906 915 975 9 96 317 NFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSQBGFSAAITSNGPLLSTVGSYDWAG PVLAVKAIMBFNPREVARNVFECNDQVVXGKGAGEVRVCLHVQKSTRDRLREGQIQSVVT SLVGTPLSAFGNLRPVLAEDAQREFTALPPFEXNCGNDNICQDDLSITFSFMSLDCLVVG GPREFAVTVTVRNDGEDSYRTOVTFFFPLDLSYRKVSTLONGRSORSWRLACBSASSTEV QLELPVKYAVYVTSHGVSTKYLAFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV RINOTVIWDRPOVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCORIOCDIP RINOTATMDR POVITS ENLISSING THE REPLANTANCE AVOID TO THE REPLANTANCE AVOID TO THE REPLANTANCE AND THE REPL PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF RIHFTFKEFONNPNPRSLIKPITOLLGRIHTATGLRKVVRELFNITNGARKNAFKILFLL RIHFTFKEFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI TOGEKFGDPLGYEDVI PELDREGVIRYVLGFGDAFRSEKSRQELMTVASKPPRDHVFQAN NFEALKTVQNQLREKI FAI BGTQTGSSSSFEHEMSQBGFSAAITSNGPLLSTVGSYDWAG GVFLYTSKEKSTFINYFRVDSDMNDAYLGYAAAIILRNRVOSLVLGAPRYQHIGLVAMFR ONTCHWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL QNTGWWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL PRGORARWOCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVALGAPGBEDNRGAVYLF HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 556 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ PVLRVKAIMEFNPREVARNVFBCNDQVVKGKEAGBVRVCLHVQKSTRDRLREGQIQSVVT SLVGTPLSAFGNLRPVLAEDAQRIFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SGALKSTSCSINHPI PPENSEVTFNI TFDVDSKASLGNKLLLKANVTSENNMPRTNKTEP QLELPVKYAVYMVVTSHGVSTKYLNPTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV RLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEBF FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQETVAANQRGSLYQCDYSTGSCEPI Gaps ij Length 1152; Indels DB 1, Š Score 5823.5; Pred. No. 0; 8; Mismatches 99.1%; 98.8%; Matches 1123; Conservative Similarity . 929 736 856 916 916 257 437 481 497 541 601 616 661 721 781 964 901 196 Н 17 77 121 137 181 197 241 301 361 377 421 841 Query Match Best Local (61 셤 å 9 d 8 ે 셤 d g ති රි g Š 셤 ठे g ò q õ ò ઠે Ω̈́ 8 a ℰ g ठ 8 δ ŝ ŝ 8 ે

SEQUENCE OF 17-28.

**X MEDLINE=85188276; PubMed=3887182;

**X Springer T.A., Teplow D.B., Dreyer M.J.;

**Sequence homology of the LPA-1 and Mac-1 leukocyte adhesion

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Mature 314.540-542 [1985].

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**Mature 314.540-542 [1985].

**Sequence homology of the LPA-1 and Mac-1 leukocyte interferon.";

**A WELL AS IN MEDIATING THE PUPAKE OF COMPLEARMY-COATES.

**A WELL AS IN MEDIATING THE RECEPTOR FOR THE ICIB FRAGMENT OF THE THIRD COMPLEMENT COMPONENT. IT RECOGNIZES THE R-G-D PEPTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR FREINOGEN GAMMA CHAIN. ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR CAMPAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-MEDIATED OF THE ALPHA-M GHANN GHAIN. ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN GUIGNATIVE CHARLES IN NEUTROPHILA ACCOMPLANTICN, IN RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT ORDER DEVELOP CHARLES AND CHARLES MICE BEVELOP CHARLES AND CHARLES THE CAMPASTANT THESE MICE DEVELOP CHARLES THE CAMPASTANT THE C SWISS-PROT entry is copyright. It is produced through a collaboration 1036 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTBT 1095 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFPKRQYKDMMSEGGPPGAEPQ 1137 GRANULOCYTES.

DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWPA DOMAIN. INTEGRINS 01-NOV-1988 (Rel. 09, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 1ntegrin alpha-M precursor (Cell surface glycoprotein WAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI). "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Wallebrand factor."; EMBO 0.7:1371-1378(1988). KVEPFEVPNPLPLIVGSSVGGLLILALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ STRAIN=BALB/C; TISSUB=Spleen;
MEDLINE=86287312; PubMed=2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.,
"A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986). Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus. ASSOCIATES WITH BETA-2. SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 1 VWFA domain. SIMILARITY: Contains 7 FG-GAP repeats. I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE AA 1153 SEQUENCE FROM N.A. MEDLINE-88312584; PubMed=3044779; Bukaryota, Metazoa; Chordata; Mammalia, Butheria; Rodentia; NCBL_TaxID=10090; FROM N.A. STANDARD; Mus musculus (Mouse) SEQUENCE OF 11-45 OBESITY ITAM MOUSE P05555; Pytela R.; 1081 1096 ITGAM. ITAM MOUSE This g 8 a

PPGIQEBFNATLKGNLSPDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTBT

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PLQVPPEAVNMSLGISLAVSTVPQQILACGPTVHQNCKENTYVNGLCYLFGSNLLRPPQQ

17 121 PPEALRECPQQESDIVFLIDGSGSINNIDFQKMKEFVSTVMEQFKKSKTLFSLMQYSDEP RIHFTFKEFONNPNPRSLIKPITQLLGRTHTATGLRKVVRBLFNITNGARKNAFKILFLL

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PPBALRGCPQBDSD1AFLIDGSGS11PHDFRRMKBLVSTIMEQLKKSKTLFSLMQYSBBF

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or send an email to license@isb-sib.ch).
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EXTRACELLULAR (POTENTIAL)
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REMBL; M14293; AAA39484.1; --
REMBL; M020551; S00551.
REMSP; P1215; JAA39484.1; --
REMSP; P1215; JAA39484.1; --
REMSP; P1215; JAA39484.1; --
REMSP; P1215; JACKST.
REMSP; P1215; JACKST.
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REMSP; PR00193; INTEGRINA.
REMSP; PR00195; INTEGRINA.
REMSP; PR00195; INTEGRINA.
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CYTOPLASMIC (POTENTIAL)
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FG-GAP 2.

WPA.

FG-GAP 3.

FG-GAP 3.

FG-GAP 5.

FG-GAP 5.

FG-GAP 6.

FG-GAP 6.

FG-GAP 7.

FG-GAP 6.

FG-GAP 6.

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FG-GAP 7.

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480

496 540 552 600 615 660 675 735 780 795 839 855 899

376 420 436

117 NFEALNTIQNQLQEKIFALEGTQTGSTSSFEHENSQEGFSASITSNGFLLGSVGSFDWAG

NFEALKTVONOLREKI PAI EGIOTGSSSSFEHEMSOEGFSAAITSNGPLLSTVGSYDWAG

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GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR

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PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA.I GAPGBEDNRGAVYL.F

HCTSGSGISPSHSQRIAGSKLSPRLQYFCQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ

PVLRVKAIMEFNPREVARNVPBCNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT

SLVGTPLSAFGNLRPVLAEDAQRLFTALPPFEKNCGNDNICQDDLSITFSFMSLDCLVVG TLVGEPLRSFGNLRPVLAMDAQRFFTAMFPFRKNCGNDSICQDDLSITMSAMGLDTLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRL-ACESASSTE

YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIBDPVSPIVLRLMF

TDGEKFGDPLGYEDVI PELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN

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VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDI 1019
                                                                                                                                                                     PSFNTQBIFNVTLKGNLSPDWYIKTSHGHLLLVSSTBILFNDSAFALLPGQESYVRSKTB 1095
                                                                                                                                                                                                               PPPGIQERFNATLKGNLSFDWYIKTSHNHLLIVSTARILFNDSVFTLLPGQGAFVRSQTF 1079
                                                                                                                                                                                                                                                                     TKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGPPKRQYKDMMSEGGPPGAEPQ 1137
840 VSGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTE
                                                                                                PQLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVPLVP
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                                                                                                                                                                                                                            Length 1153;
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Best Local Similarity 73.5%; Pred. No. 1.5e-292;
Matches 836; Conservative 147; Mismatches 153; Indels
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MEDLINE=87167596; PubMed=3549901;

MEDLINE=87167596; PubMed=3549901;

MIJIET L.J., Wiebee M., Springer T.A.;

MIJIET L.J., Wiebee M., Springer T.A.;

MIJIET L.J., Wiebee M., Springer T.A.;

"Purification and alpha subunia N-terminal sequences of human Mac-1

"I mand p150,95 leukocyte adhesion proteins.";

"I mand p150,95 leukocyte adhesion proteins.";

"I mentant IN MIDGOTHE ADHESION AND CHEMOTAXIS.

"INTERACTION INTRING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

IMPORTANT IN MONOCYTE ADHESION AND CHEMOTAXIS.

"SUBUNIT: HETERODINGE OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X

ASSOCIATES MITH BETA-2.

"SUBUNIT: HETERODINGE OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X

ASSOCIATES SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND GRANULOCYTES.

"I SUBULIANTLY: Contains I TOOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRING WITH I DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

"SIMILARITY: Contains I VWFA domain."

"SIMILARITY: Contains 7 PG-GAP repeats.

"SIMILARITY: Contains 7 PG-GAP repeats.
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                                                                                                                                                                                                                                              SEGUENCE FROM N.A.
MEDLINE=88166645; PubMed=3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.,
"CDNA cloning and complete primary structure of the alpha subunit of
a leukcorte adhesion glycoprotein, p150,95.",
EMBO J. 6:4023-4028(1987).
                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
ITGAX OR CD11C.
                                                                                                                                                                    Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corbi A.L., Garcia-Aguilar J., Springer T.A.,
J. Biol. Chem. 265:12750-12751(1990).
                                         PRT; 1163 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         . Biol. Chem. 265:2782-2788(1990)
                                         STANDARD;
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                                        ITAX HUMAN
P20702;
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61 RIQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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1163 AA; 127885 MW; 6C4E19CC3F62A473 CRC64;
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EMBL, M29486; AAAS1620.1; JOINED.
PR, AA6584; RWHUIC.
PDB; IN3Y; 18-PEB-03.
Genew; HGNC:6152; ITGAX.
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(Rel. 41,

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                        RIHFTFKEFONNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
                                           QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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TTAD_HUMAN STANDARD; PRT; 1162 AA Q1349; Q15575; Q15576; Created) 16-0CT-2001 (Rel. 40, Last sequence update)
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SUBCRIATES WITH BETA-2.
SUBCRIATES WITH BETA-2.
SUBCRIADAR LOCATION: Type I membrane protein.

IISSUB SPECIFICITY: EXPRESED MODERATELY ON MYBLOMONCYTIC CELL
LINES AND SUBSETS OF PERIFHERAL BLOOD LEUKCYTES AND STRONGLY ON
TISSUB-SPECIFICITY EXPLAINER RED FULP MACROPHAGES.
ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED FULP MACROPHAGES.
NOTH I-DOMAIN: THE INTEGRIR I-DOMAIN (INSERT) IS A WHY DOMAIN. INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Contains 1 WPRA domain.
SIMILARITY: Contains 1 WPRA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH VCAMI.

MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                MEDLINE-56111956; PubMed=8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
"A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-235 FROM N.A.
MEDLINE-20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Structural and functional characterization of the leukocyte integrin gene CD14d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
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INTERACTION WITH VCAM1.

MEDLINE-99370062; PubMed=10438935;
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Garliner B.S., Gallatin W.M., Staunton D.B.;
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.B.;
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1.",

J. Immunol. 163:1984-1990(1999)

-! FUNCTION: INTEGRIN ALPHA-D/BSTA-2 IS A RECEPTOR POR ICAM3 AND VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS CLEARING LIPOPROTEINS FROM PLANDUSS AND IN PHAGGOSTOSIS OF BLOODBORNE PARTHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
annotation update)
(Leukointegrin alpha D) (CD11d) (ADB2)
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROM
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                   ntegrin alpha-D precursor TGAD.
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[2]
                                                           sapiens (Human).
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NCBI_TaxID=9606;
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                                                                                                                                                             SECUENCE
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Ouery Match 57.6%; Score 3388; DB 1; Best Local Similarity 58.9%; Pred. No. 6.7e-221; Matches 665; Conservative 168; Mismatches 288;

Length 1162;

481

RIQVPVEAVNMSIGLSLAATTSPPQILACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120

FNLDVEEPTIPQEDAGGPGQSVVQFGGSRLVVGAPLEVVAANQTGRLXDCAAATGMCQPI

FNLDTENAMTPOENARGFGOSVVQLQGSRVVVGAPQBIVAANQRGSLYQCDYSTGSCEPI

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VRINGTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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XX XEDINES-99425288; PubMed=10493822; Xellen J., Weltz-E-Schmidt G., Ramage P., Geyl D., Kriwacki R., Legge G., Cottens S., Weitz-Schmidt G., Hommel U.; Cottens S., Weitz-Schmidt G., Hommel U.; Colla I-domain.; Colla I-domain.; Setuctural basis for LFA-1 inhibition upon lovastatin binding to the Colla I-domain.; Colla I-domain.
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SEQUENCE PROM N.A. (ISOPORM 2).

Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,

Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,

Enhrmann J., Mason T., Crosby M.E., Barnstead M., Cronin L.,

Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

Eichler B.E., Harris P.C., Venter J.C., Adams M.D.;

Genome duplications and other features in 12 Mo of DNA sequence from human chromosome 16p and 16q.";

Genomics 60:295-308(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDLINE=89139587; PubMed=2537322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
                                                                                                                                                                                                                                                      TTAL HUMAN STANDARD; PRT; 1170 AA.
P20701; 043746;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-ccT-2003 (Rel. 42, Last annotation update)
11-cgrin alpha-L precursor [Leukocyte adhesion glycoprotein LFA-1 alpha chain) (Leukocyte function associated molecule 1, alpha chain)
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"The role of the divalent cation in the structure of the I domain from the CD11a/CD18 integrin.";
Structure 4:931-942(1996).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 153-335.
MEDLINE=96398682; PubMed=8805579;
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IsoId=P20701-2; Sequence=VSP_002738;
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J. Cell Biol. 108:703-712(1989).
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ITGAL OR CD11A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Note=No experimental confirmation available;
-! TISSUE SPECIFICITY: LEUKNOCYTES.
-! DOMAIN: THE INTEGRIN I-DOMAIN GREETS IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS TO NOT UNDERCO PROTEASE CLEAVAGE.
-! SIMILARITY: Belongs to the integrin alpha chain family.
-! SIMILARITY: Contains 1 VWFA domain.
-! SIMILARITY: Contains 1 VWFA domain.
-! DATABASE: NAME-PROW; NOTE-CD guide CD11a entry;
-! MWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMEL, YOO756; CAA66747.1, -

REMEL, AC002310, AAC31672.1; -

REMEL, ACCO02310, AAC31672.1; -

REMEL, ACCO02310, AAC316.0

REMEL, ACCO02310, AAC316.0

REMEL, ACCOO.

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FG-GAP 5.
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                                                                                  RGGOVSVCPLPRGORARWQCDAV - LYGEQGQPHGRFGAALTVLGDVNGDKLTDVAIGAP
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                                                        SYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQH
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01-MRR-1992 (Rel. 21, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
11ntegrin alpha-i precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (Leukocyte function associated molecule 1, alpha chain)
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TTGAL OR LFA-1.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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R -> W (IN REF. 1 AND 2)
Y -> I (IN REF. 2).
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                                                                                                                                                                                                  MEDLINE-85188276; PubMed=3887182;
MEDLINE-85188276; PubMed=3887182;
MEDLINE-85188276; PubMed=3887182;
MEDLINE-85188276; PubMed=3887182;
Sequence homology of the LieA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon.";
Nature 314:3640-542 [1985].
-!- FUNCTION: INTEGRIN ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAM1, ICAM2, ICAM3 AND ICAM4. IS INVOLVED IN A VARIETY OF IMMUNE PHENOMENA INCLUDING LEUKOCYTER-ENDOTHELIAL CELL INTERACTION, CYTOTOXIC T-CELL MEDIATED KILLING, AND ANTIBODY DEPENDENT KILLING BY GRANULOCYTES AND MONOCYTES. MICE EXPRESSING A NULL MOTATION OF THE ALPHA-L STBUNIT CRAN DEMONSTRATE IMPAIRED TUMOR REJECTION AND IMPAIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEUCOCYTES RECRUITMENT.
SUBBUNIT: HETRRODIMER OF AN ALPHA AND A BETA SUBUNIT, ALPHA-L
ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: LEUKOCYTES.
DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOWAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 VWFA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
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R HSSP; P20701; LTS-

R HSSP; P20701; LTS-

R MCD; MGI:96606; Itgal.

R InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR0000413; Integrin_alpha.

R Fam; PP00189; PC-CAP, 3.

R Fam; PP00189; PC-CAP, 3.

R PROMIS; PR0185; INTEGRINA, BRINTS; PR0195; INTEGRINA.

R RANAT; SM00191; Int_alpha; 5.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.

R PROSITE; PSS0242; INTEGRIN_ALPHA; 1.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                               MEDLINE=91268576; PubMed=2051027;
Kaufmann Y., Tseng B., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
alpha-subunit and its expression in COS cells.";
". Immunol. 147:369-374(1991).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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VFG-GAP 3.
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FG-GAP 6.
FG-GAP 7.
PG-GAP 7.
PG-GAP 7.
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                                                                                                                                                                                                                                                                                                                                                                             89; Gaps
                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   Query Match 25.8%; Score 1516.5; DB 1; Length 1163; Best Local Similarity 33.9%; Pred. No. 2.6e-94; Matches 396; Conservative 216; Mismatches 466; Indels 89;
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1051 IVSTABILFNDSVFTLLPGQGAFVRSQTBTKVBPPBVPNPLPLIVGSSVGGLLLLALITA 1110
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SPIVLRLNFSLV---GTPLSAFGR-LRPVLAEDAQRLFTALFPFEROCGNDNICQDDLSI 767
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                                                      CRILANLSYTLQLDGHRWRSRGLFPDGSHELSGNTSITP-DKSCLDFHFHFPICLQDLI
                                                                                                     SSPARS-----GPLRLMSSASLAVEWTLSNSGEDAYWVRLDLDFPRGLSFRRVEMLQ-
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Integrin alpha-E precursor (Integrin alpha M290). ITGAE. musculus (Mouse) SEQUENCE FROM N.A. NCBI_TaxID=10090; Mus

SUBUNIT: HEFERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAINS LINKED BY A DISULFIDE BOND. ALPHA-E ASSOCIATES WITH BETA-7.
SUBCELLULAR LOCATION: Type I membrane protein. --1

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-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains I VWFA domain.
-!- SIMILARITY: Contains 7 FG-GAP repeats. (POTENTIAL).
(POTENTIAL). POTENTIAL.
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GEU-RIGH (ACIDIC).
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BY GLCNAC. (GLCNAC. FG-GAP 7. POTENTIAL. POTENTIAL. FG-GAP 3. FG-GAP 4. FG-GAP 5. FG-GAP 6. LINKED MGD; MGI:1298377; Itgae. InterPro; IPR000413; Integrin_alpha. InterPro; IPR002035; VWF_A. EMBL; U12236; AAC52142.1; -. HSSP; P11215; 1A8X. DISULPID DISULPID DISULPID DISULFID DISULFID CARBOHYD DISULFID CARBOHYD CARBOHYD CARBOHYD CARBOHYD REPEAT REPEAT REPEAT CA BIND CA BIND CA BIND CA BIND DOMAIN CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD

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986 KERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIPFFGIQBEFNATLKGNLSFDWYIKTS 1045
                                                                                                                                                                                                  1046 HNHLLIVSTA-----EILFNDSVFTLLPGQGAFVRSQTETKVBPF----EVPNPLPLIV 1095
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12 SEQUENCE FROM N.A., AND SEQUENCE OF 19-38 AND 179-188.

13 SEQUENCE FROM N.A., AND SEQUENCE OF 19-38 AND 179-188.

14 SEQUELLE-Leukemia, and Lymphocytes;

15 Shaw S.K., Cepek K.L., Murphy B.A., Russell G.J., Brenner M.B.,

16 Parker C.M.,

17 Paloi. Chem. Cloning of the human mucosal lymphocyte integrin alpha E. RT.

18 Subunit. Unusual structure and restricted RNA distribution.";

17 Subunit. Chem. 269:6016-6025(1994).

18 REVISIONS TO 88-114.

19 REVISIONS TO 88-114.

19 REVISIONS TO RAH.

10 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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TISSUB-Fetal kidney,
TISSUB-Fetal kidney,
TISSUB-Fetal kidney,
TISSUB-Fetal kidney,
Touchman J.M., Anikster Y., Dietrich N.L., Maduro V.V., McDowell G.,
Shotelersuk V., Bouffard G.G., Beckstrom-Sternberg S.M., Gahl W.A.,
Green B.D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genomic region encompassing the nephropathic cystinosis gene (CTNS): complete sequencing of a 200-kb segment and discovery of a novel gene within the common cystinosis-causing deletion."; Genome Res. 10:165-173(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P38570; Q9NZU9;
30-OCT-1994 (Rel. 30, Created)
30-MAY-2000 (Rel. 30, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
antigen) (CD103 antigen) (Integrin alpha-IEL).
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                   | REGISTATION | CONTENTION | CO
SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED ON A SUBCLASS OF T-LYMPHOCYTES KNOWN
AS INTRA-EPITHELIAL LYMPHOCYTES WHICH ARE LOCATED BETWEEN MUCOSAL
BPITHELIAL CREES.

DOMAIN: THE INTEGRAIN I-DOMAIN (INSERT) IS A VWPA DOMAIN. INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains I VWPA domain.
DAITABASE: NAME-PROW; NOTE-CD guide CD103 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd103.htm".
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19.2%; Score 1128; DB 1; Length 1179;
Best Local Similarity 28.7%; Pred. No. 5.1e-68;
Matches 338; Conservative 213; Mismatches 454; Indels 172; Gaps
(POTENTIAL).
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1 BUDDIAL: ";
2 Biol. Chem. 26812899-2996 (1993)
2 Biol. Chem. 26812899-2996 (1993)
3 Biol. Chem. 26812899-2996 (1993)
4 Biol. Chem. 2681289-2996 (1993)
5 COLLAGEN. IT RECORNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-
B-R IN COLLAGEN.
5 B-R IN COLLAGEN.
6 B-R IN COLLAGEN.
7 SEQUENCE GASOLINE: ALPHA AND A BETA SUBUNIT. ALPHA-1
ASSOCIATES WITH BETA-1.
6 L- SUBCELLULAR LOCATION: Type I membrane protein.
7 L- DOMAIN: THE INTEGRIN. 1-OMAIN. (INBERI) IS A VWFA DOMAIN. INTEGRINS
8 NITH 1-DOMAINS DO NOT UNDERSO PROTEASE CLEAVAGE.
1- SIMILARITY: Contains 7 FG-GAP repeats.
2 SIMILARITY: Contains 7 FG-GAP repeats.
2 SIMILARITY: Contains 7 FG-GAP repeats.
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4 SIMILARITY: Contains 7 FG-GAP repeats.
5 SIMILARITY: Contains 7 FG-GAP repeats.
6 SIMILARITY: Contains 7 FG-GAP repeats.
7 FFR: A45226; A45226.
7 FFR: A45226; A45526.
7 FFR: A65226; A45526.
7 FFR: A65226; A45226.
7 FFR: A65226; A65226.
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7 FFR: A66226; A6526.
7 FFR: A66226; A66226.
7 FFR: A66226; A
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                                                                                                                                                                                                                                                                                           1038 FDWYIKTSHNHLLIVST-----ABILFNDSVFTLLFGGGAFVRSQTETKVBFFEVPNPL 1091
                                              PPLDLSYRKVSTLQMQRSQRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNI 866
                                                                                                       874 YPRNLQ-----LKRMQKPPSPNIQCDDPQPV---ASVLIMNCRIGHPVL-KRSSAHVSV 923
                                                                                                                                                 867 TEDVDSKASLGNKLLLKANVTSENN----MPRTNKTBFQ---LELPVKYAVYMVTSHGV 919
                                                                                                                                                                     S--TKYLNPTASENTSRVMQHQYQVSNLGQRSLPISLVPLVPVRLNQTVIWDRPQVTPSE 977
757 SGSQLCEDL-LLMPTEGELCEEDCPSNASVKVSYQL-QTPEGQTDHPQP1LDRYTEPFAI 814
                             ALPPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRIQVTFF 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. PubMed=8428973; MEDLINE=93155124; PubMed=8428973; Briesewitz R., Epstein M.R., Marcantonio B.B.; Meriesewitz R., Epstein M.R., Marcantonio B.B.; MExpression of native and truncated forms of the human integrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a)
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GO: GO:0004895; F:cell adhesion receptor activity; NAS.
GO: GO:0005518; F:collagen binding; TAS.
GO: GO:0005160; P:cell-matrix adhesion; NAS.
InterPro; IPR000413; Integrin alpha.
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18.5%; Score 1085.5; DB 1; Length 1151; 27.6%; Pred, No. 3.7e-65; Live 209; Mismatches 488; Indels 201; Gaps
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BY SIMILARITY.

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
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Db 11.	RESULT 10 ITAH HUMAN ID ITAH HI			OC Mammal OX NCBI_TP RN [1] RP SEQUENC	RC TISSUE: RX MEDLIN RA Lehner(_			7	1	÷ ÷			CC or send CC	DR EMBL; DR HSSP; DR Genew;	DR GO; GO DR GO; GO
:: :: ::	167SKTLFSLMOYSBEFRIHFTFKEFQNNFNPRSLIKPITQLLGR-THTATGLKKVR 220 :	221 ELFNITNGARKNAFKILFLLTDGEKFGDPLGYEDVIPBLDREGVIRYVLGFGDAFR 276	277 -SEKSRQELATVASKPPRDHVFQANNFEALKTVQNQLREKIFAIBGTQTGSSSSFEHEMS 335	336 QBGFSAAITSNGPLLSTVGSYDWAGGVPLYTSKEKGTF-INMTRUDSDMUDAYLG 389	390 YAAAIILRNRYQSL-VLGAPRYQHIGLVAMFRQNTGWMESNANVKGTQIGAYFGASLCSV 448 	449 DVDSNGSTDLVLIGAPHYYEQTR-GGQVSVCPLPRGQRARWQCDA 492	493 VLYGEGGOPWG-RFGAALTVLGDVNGDKLIDVAIGAPGEBDNRGAVYLFHGTSGSGISPS 551 ::	552 HSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEF 611 ::	612 NPREVARNVFECNDQVVKGKEAGEVRVCIHVQ-KSTRDRLREGGIQSVVTYDLALDSG 668	669 RPHSRAVFNETKONSTRRQTQVLGLIQTCETLKLQLFNCIEDPVSPIVLRLNFSL 722	723 VGTPLSARGNLRPVLABDAQRLFTALPPERKNCGNDNICQDDLSITFSFMSLDCLVVGGP 782	783 RB-FNVTVTVRNDGEDSYRTQVFFFFPLDLSYRKVSTLONQRSQRSWRLACESASSTEVS 841 : :: :	842 GALKSTSCSINHPIFFENSEVTENITFDVDSKASLGN-KLLLKANVISENNMPRINKTEF 900 :: :: ::	901 QLELPVKYAVYNVVTSHQVSTKYLNFTASENTSRVMQHQYQVSNLGQRS 949 :: : : : : : : : : : :	950EPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTXER 988 	989 LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPPPGIQB	1031 TLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNP 1090 :-	1091 LPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDWMSE 1128
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1 FNLDTENAMTFOENARG-FGQSVVQLQGSR-VVVGADQEIVAANQRGSLYQCDXSTGS 56			225 ITWGARKNAFKILFLITDGEKPGDPLGYEDVIPELDREGVIRYVLGRGDAFRSEK 279	280 SRQELNTVASKPPRDHVFQANNFEALKTVQNQLREKIFAIEGTQTGSSSSFEHEWSQEGF 339 313 FLABIKYIASDPDDKHFFNVTDEAALKDIVDALGDRIFSLEGTINK-NETSFGLEMSQTGF 371	340 SAAITSRUGPLLSTVGSYDWAGGVFLYTSKEKSTPINMTRVDSDWNDAYLGYAAAI 394	395 ILRNRV-QSLVLGAPRYQHIGLVAMF-RQNTGMWBSNANVKGTQIGAYFGASLCSVDVDS 452 :::	453 NGSTDLVLJGAPHYYEQTR-GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTV 511 :	512 LGDVNGDKLTDVALGAPGREDNRGAVYLPHGTSGSGISPSHSQRIAGSKLSPRLQYFQQS 571 :	572 LSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVK 629 :	630 GKBAGEVRVCLHVQKSTRDRLRBGQIQSVVTYDLALDSGRPHSRAVF 676	677 NETKNS-TRROTQVLGLTQTCETLKLQLPNCIEDPVSPIVIRLNFSLVGTPLSAFGNLRP 735	736 VLABDAQRLFTALPPFEKNCGNDNICQDDLSIT 768 :	769 FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQNQRSQRSW 828	829 RIACESASSTBVSGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTS 888 : : : : : :	889 ENNAPRTRITEPQLELPVKYAVYMVYSHGVSTKYLNFTASENTSRVMQHQYQ 941 :	VSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSD	992 IQNLGLFPIHGIMMKITIPIATRSGNRLLKLRDFLT-DEVANTSCNIMGNSTEYRFTFVE 1050 995 FLABLRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHL 1049
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GO; GO:0005518; F:collagen binding; TAS. GO; GO:0007160; P:cell-matrix adhesior; TAS. GO; GO:0007517; P:muscle development; TAS. InterPro; IPR000413; Integrin_alpha. InterPro; IPR002035; VWF.A. Pfam; PF01839; FG-GAP; 3. Pfam; PF00189; FG-GAP; 3. PRINTS; PR01185; INTEGRINA. PRINTS; PR01185; VWPADOMAIN.	SMART; SW00191; Int alpha; 5. SNART; SW00327; VWA; 1. PROSITE; PS00242; INPEGRIN ALPHA; FALSE_NEG. PROSITE; PS00244; VMFA; 1. PROSITE; PS00244; VMFA; 1.	Acceptor; Grycopiocein; Iransmenbrane; Magnesium; Polymorphism. POTENTIAL.	INTEGRIN ALPHA-11. EXTRACELLULAR (POTENTIAL) POTENTIAL: COMPART (POTENTIAL)	FG-GAP 1. FG-GAP 2. VWFA.	FG-GAP 5. FG-GAP 5. FG-GAP 6.	FG-GAL /. POLY-LEU. POLY-ARG. POTENTIAL.	POTENTIAL. BY SIMILARITY. POTENTIAL.	POTENTIAL, BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.	AC	77 7 7		AC	v -> M. V -> M. FTId=VAR_009889. R -> L. /FTId=VAR_009890.	L -> P. /FTId=VAR_009891. I -> M. /FTId=VAR_009892.	Missing.	MW; 60303C08A4A4CD52 C	- 13
:collagen :cell-matr: :muscle der 13; Integri 35; VWF_A. -GAP, 3. a; 1. INTEGRINA.	SM00191; Int_alpha; 5 SM00327; VWA; 1. B; PS00242; INTEGRIN_A: F; PS50234; VWFA; 1.	alcium; 22		•	, y y y to i	1162 1177 496	6 1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	159 668 789 787	893 82 95 291	331 449 469	6 6 4 2 8 8 5 7 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	973 1032 1040	433 524	972 1003	1030	; 133609	28.3\$ vative
005518; F 007510; P 007517; P 1 IPR00004 11839; FG 10092; VW	400191; I 400327; V PS00242; PS50234;	Repeat; C	11 23 1143 143	102	5322	1154 1174 488	613 76 121		7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 4 4 1 8 8 4 6 6 1 8 9 5 6	528 642 694 857	973 1032 1040	433 524	972	1030	1189	Simi 9;
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REQUENCE FROM N.A.

**REDINES-94193647; bubMed=7511592;

**MEDINES-94193647; bubMed=7511592;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata T ., Puzon W ., Takada Y .;

**Amata N ., Collage V ., Puzon W ., Puzon M .;

**Amata T ., Puzon W ., Puzon M ., Puzon M .;

**Collage W ., Puzon M ., Puzon M .;

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1050 LIVSTABILFNDSVFTLLPGQGAFVRSQTBTKVEPFEVPN-----PLPLLVGSSVGGLL 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa)
(Collagen receptor) (VLA-2 alpha chain) (CD49b) (Fragment).
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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18 1170 1170 1171 1170 1170 1170 1170 11	imilarity 27.5%; Pr. ; Conservative 218; ; Conservative 218; ;: :
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MEDLINE-94363406; PubMed-8081889; Edelman J.M., Chan B.M., Uniyal S., Onodera H., Wang D.Z., Danjanovich, L., Latzer D.B., Finberg R.W., Bergelson J.M.; im, im, im, im, im, in, in, in adhesion but not virus binding.";

not virus binding."; Cell Adhes. Commun. 2:131-143(1994)

SEQUENCE OF 450-1178 FROM N.A. INSUBELINES, MEDIINE=94355691; PubMed=7521231; Wu J.E., Santoro S.A.;

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430 VASISTGNSVHFVAGAPRANYTGQIVLYSVN----ENGNVTVIQSQRGDQIGSYFGSVL 484
                                                                                                   CSVDVDSNGSTDLVLIGAPHYYEQTR - - GGOVSVCPLPRGQRARWQCDAVLYGEQGQPWG 503
                                                                                                                                                                                                                                                                                                                                                   SPRIQYEGOSISGGODITMDGLVDITVGAQGHVILLIRSQPVIRVKAIMEFNPREVARNVF 621
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TITAZ MOUSE STANDARD; PRT; 1178 AA.

10-01-1998 (Rel. 36, Created)

15-01-1998 (Rel. 36, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Integrin alpha-2 precursor (Platelet membrane glyc (Collagen receptor) (VLA-2 alpha chain) (CD49b).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; X75477; CAA53178.1; -.
BIR; S44142; S44142.
BISSP, P17301; 1AOX.
MGD; MGIS6600; IEQA2.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR0002035; VWF_A.
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glycoprotein Ia) (GPIa)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090;

Mus musculus (Mouse)

CBA; TISSUE-Lung;

[1] SEQUENCE FROM N.A. STRAIN=C57BL/6 X C

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985 LVTIHIPQYTKEKNPLLYLTGIQTDQAGDISCTAEINPLKLPHTA----PSVSFKNENFR 1040
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EAYSETUKVPSIPFYKEGGSDGICISDLILDVQQLFALQTQSF----IVSNQNKRLTFS
                                                        981 STCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEFFNATLKGNLSFDW
                                    VTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKST
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Santoso S., Kalb R., Walka M., Kiefel V., Mueller-Eckhardt C.,
Newman P.J.,
"The human platelet alloantigens Br(a) and Brb are associated with a
"The human platelet alloantigens Br(a) and Brb are associated with a
single amino acid polymorphism on glycoprotein Ia (integrin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98019223; PubMed-9353312;
Emsley J., King S.L., Bergelson J.M., Liddington R.C.;
"Crystal structure of the I domain from integrin alpha2betal.";
J. Biol. Chem. 272:28512-28517(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein Ia)
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and the presence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
NCBL_TaxID=9606,
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01-AUG-1990 (Rel. 15, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11-Grin alpha-2 precursor (Platelet membrane g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89308879; Pubmed=2545729;
Takada Y., Hemler M.E.;
The primary structure of the VLA-2/collagen
(platelet GF18): homology to other integrins
D. Cell Biol. 109:397-407(1989).
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17.9%; Score 1054; DB 1; Length 1181;
Best Local Similarity 26.8%; Pred. No. 5.2e-63;
Matches 328; Conservative 215; Mismatches 494; Indels 188; Gaps
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996 YIKEKNPLMYLTGVQTDKAGDISCNADINPLKIGQT----SSSVSFKSENFR---HTKE- 1047
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                                                                                                                                                                        225 ITWGARKNAFKILFLLTDGEKFGDPLGYEDVIPELDREGVIRY---VLGF--GDAFRSEK
                                                                                                                                                                                                                                                               SAIAALSDINMDGFNDVIVGSPLENQNSGAVYIVNGHQGT-IRTXYSQKILGSDGAFRSH
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                                   108 FLFGSNIRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLK--
                                                                150 SDISPDF-OLSASFSPATOPCPSL-IDVVVVCDESNSIYPWD--AVKNPLEKFVQGLDIG
                                                                                                     166 KSKTLFSLMQYSEEFRIHFTFKEPQNNPNPRSLIKPITQLLG-RTHTATGLRKVVRELFN
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NEARY CRYSTALLOGEAPHY (2.1 ANGSTROMS) OF 151-364.

NEDLINE-99313197; PubMed=10386526;

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Gotwals P.J., Karpusas M.; enhalment integrin I-domain: insights into integrin I-domain function.";

FEBS Lett. 452:379-385(1999).

--- FINCTION: INTEGRIN ALPRA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-P-G-
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90338125; PubMed=2380249; Ignatius M.J., Large T.H., Houde M., Tawil J.W., Barton A., Bsch P., Carbonetto S., Reichardt L.F.; Resch P., Carbonetto S., Reichardt L.F.; Esch P., Carbonetto S., Reichardt D.F.; Integrin alpha 1-subunit: a receptor for laminin and collage...; J. Cell Biol. 111:709-720(1990).
                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
11-NOV-1990 (Rel. 42, Last annotation update)
111-GCT-2003 (Rel. 42, Last annotation update)
(VLA-1)
(CD49a).
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
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EXTRACELLULAR (POTENTIAL)
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us-09-902-481b-3.rsp

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989 RKRGHFPMPELQLSISFPNLTADGYPVLYPIG-----WSSSDNWNCRPRSLEDPFGINS 1042
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                                                                                                                                                             TVNSATIPGDVLXIAGOPRYNHTGQVVIYKMEDGNINILQTLQTEQTGBYFGSVLTTIDI
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|VRIPSGGDGKTLKFFGQSIHGEMDLNGDGLTDVTIGGLGGAALFWARDVAVVKVTMNFEP
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                                            QEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMND---AYLGY
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
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TISSUE-ACCIDENCE FROM N.A.

TISSUE-ACCIDENT PubMed=10702680;

MEDLINE=20169197; PubMed=10702680;

Lehnert K., N. J., Lendy B., Gough S.M., Morris C.M., Eiu D.,

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Lehnert K., N. J., Landy B., Gough S.M., Morris C.M., Eiu D.,

Mang S.-X., Landy P.R., Krissansen G.W.;

The integrin alpha10 subunit: expression pattern, partial gene

structure, and chromoscal localization.,

Confedent alpha10 subunit: 153 A RECEPTOR FOR COLLAGEN.

L. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-10

ASSOCIATES WITH BETA-1.

C. ISUBURIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-10

ASSOCIATES AND ALPHA AND A BETA SUBUNIT. ALPHA-10

C. ISUBURIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-10

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EMBL; AF112345; AAF21944.1; -.
EMBL; AF712723; AAF61638.1; -.
HSSP; P17301; 1AOX.
Genew; HGNO:6135; ITGA10.
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TISSUE=Articular chondrocytes;
TISSUE=Articular chondrocytes;
MEDILINE=98152078; PubMed=9685191;
Camper L., Hellman U., Lundgren-Adkerlund E.;
"Isolation, cloning, and sequence analysis of the integrin subunit alpha10, a beta1-associated collagen binding integrin expressed on
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                    chondrocytes.";
J. Biol. Chem. 273:20383-20389(1998)
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83 NAPCAKGHLGDYQLGNSSHP------AVNWHLGMSLLETDGDGGFWACAPLWSRACGS 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ------DYSTG-SCEPIRLOVPVEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSE
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Query Match 17.7%; Score 1042.5; DB 1;
Best Local Similarity 28.5%; Pred. No. 3e-62;
Matches 34%; Conservative 201; Mismatches 495;
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661	919	715	734	768	786	825	846	874	898	931	943	975	991	1024	1051	1084	1111	1143		
ASMPHALSYFGRSVDGRLDLDGDDLVDVAVGAQGAAILLSSRPIVHLTPSLBVTPQAİSV	9 NVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVF	VQRDCRRRGQEAVCLTAALCFQVTSRTPGRWDHQFYMRFTASLDEWTAGARAAF	NET - KNSTRROTOVLGLTOTCETLKLOLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLR	GGGGRLSPRIRLSVG-NVTCEQLHFHVLD-TSDYLRPVALTVTFALDNTTKPG	PVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPR3FN	PULNEGSPISIQKLVPFSKDCGPDNECVTDLVLQVNMDIRGSRKAPFVVRGGRRKVL	VIVIVRNDGEDSYRTQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKS		TSCSINHPIFPENSEVTFNITFDVDSKASLGLKANVTSENNMPRTNKT	RICSVGHPVFQTGAKVTFLLEFEFSCSSLLSQVFGKLTASSDSLERNGTLQENTAQT	BPQLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVS	: : : : : : : : : :	NLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPS	NLGCYVVSGLIISALLPAVAHGGNYFLSLSQVITNNASCIVQNLTEPPG	HSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEFNATLKGNLSFDWYIKTSHNHLLI	PPVHPEELQHTNRLNGSNTQCQVVRCHLGQLAKGTEVSVGLLRLVHNEFFRRAKFXSLTV	VSTARILFNDSVFTLLPGQGAFVRSQTRTKVEPFEVPNPLPLIVGSSVGGLLLLALITAA	VSTRELGTEEGSVLQLTEASRWSESLLEV-VQTRPILISLWILIGSVLGGLLILALLVFC	: LYKLGPFKRQYK 1123	
602	9	662	677	716	735	769	787	826	847	875	899	932	944	976	992	1025	1052	1085	1112	1144
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Search completed: June 7, 2004, 17:12:42 Job time: 13.9719 secs

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Q9mzd6 bos taurus Q924w2 rattus norv Q9gk48 bos taurus

Q8cc06 mus musculu Q86g88 pseudoplusi Q80zi8 mus musculu

29tun4 oryctolagus

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

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nacione nortale de Mordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Rathallah D.M. Sr., Zerria K. Jr.;

Rathallah D.M. Sr., Zerria K. Jr.;

Rathallah D.M. Sr., Zerria K. Jr.;

Submitted (MAX-2000) to the EMBL/GenBank/DDBJ databases.

RASU; AF26859; AAF81280.1; -.

RASU; P10215; IBHQ.

R GO; GO:0004895; F:cell adhesion receptor activity; IEA.

GO; GO:0004895; F:cell adhesion receptor activity; IEA.

GO; GO:0004895; F:cell adhesion receptor activity; IEA.

RO; GO:0004895; F:cell adhesion receptor activity; IEA.

RO; GO:0004895; F:cell adhesion receptor activity; IEA.

R DITERPRO; IPR001413; Integrin_alpha.

InterPro; IPR001413; Integrin_alpha.

R Pfam; PF000357; integrin_a; 1.

R PRINTS; PR00157; integrin_a; 1.

R SMART; SM00191; Int. alpha; 5.

R SMART; SM00191; Int. alpha; 5.

R PROSITE; PS00242; INTEGRIN ALPHA; 1.

R PROSITE; PS00242; INTEGRIN ALPHA; 1.

R PROSITE; PS00242; UNFA, 1.

R PROSITE; PS00242; UNFA, 1.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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llarity 72.3%; Pred. No. 1.2e-314;
Conservative 151; Mismatches 162;
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Q8C270
Q8GB7
Q9UB90
O76378
Q9U6S1
Q9UES1
Q9BTT7
Q8BTT7
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Q91779
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0924W2
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Q8CE84
Q61989
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Matches 822; Conserv
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gallus gall
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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SEQUENCE FROM N.A.

STRAIN=C57EL/6J; TISSUE=Spinal cord;

XX MEDINE222354683; PubMed=12466851;

X The FANTOM Consortium,

The RIXEN Genome Exploration Research Group Phase I & II Team;

A the RIXEN Genome Exploration Research Group Phase I & II Team;

RY The MADIANES of the mouse transcriptome based on functional annotation of

RY GO, 770 full-length CDNAs.";

RY FOOTO FULL-Length CDNAs.";

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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          FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                             FNLDTENPMTPQENASGFGOSVIQLGETRVVVAAAQGEVKAVNQTGALYQCDYSTNRCDPI
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GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0054895; F:cell adhesion receptor activity; IEA
GO; GO:007160; P:cell-matrix adhesion; IEA.
InterPro; IPR00413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PR01895; FG-GAP; 3.
Pfam; PR00192; VAR; 1.
PRINTS; PR01185; INTEGRINA.
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                                 118 POKEPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMBOLKKSKTLFSLMQYS
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64.4%; Score 3786.5; DB 6; Length
78.4%; Pred. No. 2.7e-272;
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Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;

028984; 01-NOV-1996 (TEMBLEE). 01, Cz 01-UNN-2003 (TEMBLEE). 24, Le 01-JUN-2003 (TEMBLEE). 24, Le CD11B, (Fragment). CD11B. Sus scrofa (Pig). Sus scrofa (Pig). Bukarryora, Metazoa; Chordata; Nammalia; Eutheria; Cetartioda

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Lee J.-K., Schook L.B., Rutherford M.S.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ (1991); 140072; AAB16869.1; -. HENSP; P11215; 1BHQ.

SEQUENCE FROM N.A.

Created) Last sequence update) Last annotation update)

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960 VRLNQTVIWDRPQVTPSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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      GVFLYTSKEKSTPINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
Tsuchiya H.,
"Isolation of Genes Selectively Expressed by Dendritic Cells.";
Submitted (DEC.1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF211864; AAF23492.1;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Leukocyte adhesion glycoprotein p150,95 alpha integrin subunit.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
110-OCT-2003 (TrEMBLrel. 25, Last annotation update)
110-OCT-2003 (Human).
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO38237; A4H38337.1; -.
RGO; GO:0008105; C:integrin complex; IEA.
GO; GO:0008495; F:cell adhesion receptor activity; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WWF A.
R Pfam; PF01839; PGC-GAP, 1.
Pfam; PF01839; PGC-GAP, 1.
Pfam; PR01839; NTRGRINA.
R PRINTS; PR01185; INTEGRINA.
R PRINTS; PR01485; VWFADOWAIN.
R PRANT; SR00327; VWFADOWAIN.
R PROSITE; PS00242; INTEGRIN ALPHA; I.
R PROSITE; PS00242; INTEGRIN ALPHA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 58.8%; Score 3457; DB 4; Length 1 al Similarity 60.7%; Pred. No. 1.3e-247; 685; Conservative 143; Mismatches 295; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169 AA; 128521 MW; A17B484FEFC79EB6 CRC64;
                                                                                                                                                                                                                         DIPPFGIOEEFNATLKGNLSF 1038
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local S
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LACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSE
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                                                                                                                                                                                                                                                                                                                                                                                  1009 JAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
                                                                                                                                                                                                                                                                                                                                                                                                       1069 GOGAFVRSQTBTKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
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                                                                                                                                                                                                                     NAMPRINKTEPOLELPVKYAVYMVVTSHGVSTKYLNFTASE-NTSRVMQHQYQVSNLGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002015; VWF A.
Pfam; PF001839; FG-GAP; 3.
Pfam; PF000357; integrin_A; 1.
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54.9%; Score 3225.5; DB 11; Lengt
Best Local Similarity 57.2%; Pred. No. 2.1e-230;
Matches 645; Conservative 163; Mismatches 306; Indels
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STRAIN=Sprague-Dawley;
STRAIN=Sprague-Dawley;
O'Brien M.M.; VanderVieren M., Kilgannon P.D., Dietsch G
Gallatin W.M.;
"Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF021343, AAF21241.1;
HSSP; P11215; 1BHQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO1453; VWFADOMAIN.
SWART; SW00191; Int alpha; 4.
SWART; SW00327; VWA; 1.
PROSITE; PS00245; INTEGRIN_ALPHA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 NFDALKDIENQLKEKIPAIEGTETPSSSTFELEMSQEGFSAVFTPDGPVLGAVGSFSWSG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAFLYPSNMRPTFINMSQENEDWRDAYLGYSTALAFWKGVHSLILGAPRHQHTGKVVIFT 438
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                                                                                                                                                                                                                                                                                                                                                                                                   56.1%; Score 3297.5; DB 11; Length 1169; llarity 56.2%; Pred. No. 9.4e-236; Conservative 174; Mismatches 306; Indels 19; C
              MGD; MGI:96609; Itegax,

RGD; MGI:96609; Itegax,

RGO; GO:0008305; C:integrin complex; IEA.

RGO; GO:0008305; P:cell addesion receptor activity; IEA.

RGO; GO:0007229; P:integrin—adhesion; IEA.

RGO; GO:0007229; P:integrin—alpha.

RINTERPO; IRR004013; Integrin—alpha.

R Pfam; PF00187; Integrin—A; I.

R Pfam; PF00187; Integrin—A; I.

R Pfam; PF00187; Integrin—A; I.

R RINTS; RR0185; INTEGRINA.

R RRINTS; RR0191; Integrin—A; I.

R RRINTS; RR00191; Integrin—A; I.

R RMART; SR00191; Integrin—A; I.

R RMART; SR00191; Integrin—A; I.

R RRSITE; PR00453; VWFADOMAIN.

R SWART; SR00191; Integrin—A; I.

R RRSITE; PR00242; INTEGRIN—ALPHA; I.
                                                                                                                                                                                                                                                                                                                                                               C616412033C219A6 CRC64;
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Best Local Similarity
Matches 641; Conserv
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                                                        PEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKELVSTIMEQLKKSKTLFSLMQYSEBFR 181
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NLDVEEPIVFREDAASFGQTVVQFGGSRLVVGAPLEAVAVNQTGRLYDCAPATGMCQPIV
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25.7%; Score 1512.5; DB 11; Lengt
Best Local Similarity 33.7%; Pred. No. 5.4e-103;
Matches 394; Conservative 219; Mismatches 464; Indels
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PÉAM; PF001357; Integrin_A; 1.
PEAM; PF001257; Integrin_A; 1.
PRINTS; PR001185; INTEGRINA.
PRINTS; PR00191; Int_alpha; 5.
SWART; SW00191; Int_alpha; 5.
SWART; SW00242; INTEGRIN_ALPHA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
SEQUENCE 1161 AA; 128240 MW; 868102F7B209E431 CRC
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Last annotation update)
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STRAIN=DBA/2J; TISSUE=Spleen;
MA R.Z., Teuscher C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AF065902; AAD25885.1; --
HSSP; P20701; ILFA.
MGD; MGI:96606; ILFA.
MGD; GO:0008305; C:integrin complex; IEA.
GO; GO:0007160; P:cell adhesion receptor activity
GO; GO:007160; P:cell-matrix adhesion; IEA.
InterPro; IPR00413; Integrin alpha.
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01-NOV-1999 (TrEMBLrel.
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PROSITE; PS50234; VWFA; 1.
SEQUENCE 1160 AA; 128127 MW; A33
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                                                                           -QGAVXIFWGKPG-GLSPQPSQRIQGAQVPPGIRWFGRSIHGVKDLGGDRLADVVVGPEG 603
                                                                                                                                                                CGRITAWLSYTLQLDGHRMRSRGLFPDGSHELSGNTSITP-DKSCLDFHFHFPICIQDLI 720
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SPINVSLAFSLLEBEGTFRDQKGRAMQPILRPSIHTV-TKBIPFBKNCGEDKKCBANLTL 779
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                                                                                                          651
                                                                                                                                                  EGOIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV 711
                                                                                                                                                                                          SPIVLRLMFSLV---GIPLSAFGN-LRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSI 767
                                                                                                                                                                                                                                    TPSFMSLDCLVVGGP-----REFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQN 821
                                                                                                                                                                                                                                                         SSPARS-----GPLRLMSSASLAVEWILSNSGEDAYWVRLDLDFPRGLSFRKVEMLQ- 831
                                                                                                                                                                                                                                                                                                  -- PHSRMPVSCEEL -- TEGSSLLTKTLKCNVSSPIFKAGQEVSLQVMFNTLLNSSWEDFV 887
                                                                                                                                                                                                                                                                                                                         881 LLKANVISEN-NMPRINKIEFQLELPVKYAVYMVVISHGVSIKYLNFIASENISRVMQHQ 939
                                                                                                                                                                                                                                                                                                                                       OVLLFQAPEAGGRWNQTQXIEGTQIGSYFGGELCSVDLDQDGEAELLLIGAPLFFGEQRG
                    GOVSVCPLPRGQRARWQCDAVLYGBQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEBD
                                                             NRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLFMDGLVDLTVGAQG
                                                                                                        HVLLLRSQPVLRVKAIMEFNPRBVARNVFECNDQVVKGKEAG-EVRVCLHVQKSTRDRLR
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Spleen;
Ma R.Z., Teuscher C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EXBL; AP065901; AAD25884.1;
HSSP; P20701; 1LFA.
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GO; GO:0008305; C:integrin complex;
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01-MAY-2000 (TrEMBLE). 13,
01-JUN-2003 (TrEMBLE). 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 FRIHFTFKEF-QNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 NRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQG
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GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:000766; P:cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR0002035; WWF A.
Pfam; PF00357; integrin A; 1.
Pfam; PF00357; integrin A; 1.
Pfam; PF00185; VAA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00185; INTEGRINA.
PRINTS; SM00191; Int alpha; 5.
SMART; SM00191; Int alpha; 5.
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1160 AA; 128127 MW; A33C531B139F1FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.5%; Score 1502; DB 11;
Best Local Similarity 33.6%; Pred. No. 3.3e-102;
Matches 392; Conservative 218; Mismatches 467;
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                                                                                                           S-----SEARPCLPGV--QPRCPIVF---RWEILIQVTGTVELSKEIKAS-STLS 1045
                                                                                                                            IVSTABILFNDSVFTLLPGQGAFVRSQTBTKVEPFEVPNPLPLIVGSSVGGLLLLALITA 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                          LCSSLSVSFNSSKHFHLYGSKA-SEAQVLVKVDLIHEKEMLHVYVLSGIGGLVLLFLIFL 1104
831
                                         LLKANVISEN-NMPRINKTERQLELPVKYAVYMVVISHGVSIKYLNFIASENTSRVMQHQ 939
                                                      ELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTOQVQHV 947
                                                                     YQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQ----VTFSENLSS----TCHTKE-RLP 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                      --PHSRMPVSCEEL--TEGSSLLTKTLKCNVSSPIFKAGGEVSLQVMFNTLLNSSWEDFV
             QRSQRSWRLACESASSTEVSGAL-KSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKL
SSPARS-----GPLRLMSSASLAVEWTLSNSGEDAYWVRLDLDFPRGLSFRKVEMLQ-
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                                                                                                                                                                                                                                                       Cyprinus carpio (Common carp).

Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes,
Cyprinidae, Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                        common carp.";
                                                                                                                                                                                                                                                                                              23.5%; Score 1382; DB 13; Length 1196; 31.0%; Pred. No. 2.9e-93;
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Last annotation update)
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9; Conservative 226; Mismatches
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                                                                                                                                                                ALYKVGFFKRNLKEKMEADGGVPNGSP 1131
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                                                                                                 VSVCPLPRGQRARWQCDAV--LYGEQGQPWGRFGAALTVIAGDVNGDKLTDVAIGAPGRED
                                                                                                                      593 HVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTRDRLR
                                                                                                                                                                                                                                                                                  EGQIQSVVTYDLALDSGRPHSRAVPNBTKNSTRRQTQVLGLTQTGETLKLQLPNCIEDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823 RSQRSWRLACES--ASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALI
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Cyprinus.
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TISSUB=Peritoneal exudate cells;
Kimura M., Fujiki K., Nakao M.;
"Molecular cloning of a leukocyte integrin from the common carp.";
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Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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  ---R 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 IITDGE--ATDSGNIDAAKD-----IIRYIIGIGKHPQTKESQETLHKFASKPASBFVKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 QKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 SYKTEFDFSDYVKRKDPDALLKHVKFMLLLTNTFGAINYVATEVFREELGARPDATKVLI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 YNLDVRGARSFSPPRAGRHFGYRVLQV-GNGVIVGAPGE---GNSTGSLYQCQSGTGHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 BFRIHFTFKEFONNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIRLOVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSBNTYVKGLCFLFGSNLRQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 ANNFEALKTVONOLREKIFAIEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FNLDTENAMTFQ--ENARGFGQSYVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.8%; Score 1341.5; DB 4; Length 1086;
Best Local Similarity 32.0%; Pred. No. 2.5e-90;
Matches 374; Conservative 186; Mismatches 434; Indels 175; Gaps
                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
MCBI_TaxID=9606;
                                                                 SQTETKVEPPEVPNPLDV-GSSVGGLLLLALITAALYKLGFFKRQYKD
KYSFYEFRKDNVFSISAZLNYNTSLYNQTS-----SELKYNPH-
                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.,
Submitted (WAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (WAY-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC008777, AAM08777.1; -.
GO, GO:0004835; C:integrin complex: IEA.
GO; GO:0004835; F:cell adhesion receptor activity; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IRR002035; WW A.
Pfam; PP01839; FG-GAPP; 3.
Pfam; PP01839; FG-GAPP; 3.
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                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                               PRT; 1086
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PROSITE; PS50234; VWPA; 1.
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PRINTS, PRO1185; INTEGRINA.
PRINTS, PR00453; VWFADOWAIN.
SWART; SM00191; Int_alpha; S.
SWART; SM00327; VWA; I.
                                                                                                                                                                                                                  01-DEC-2001 (TERMBLrel. 19, 01-DEC-2001 (TERMBLrel. 19, 01-JUN-2003 (TERMBLrel. 24, Hypotherical Termblrel. 24,
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                           Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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975 EVHHSFISSYHQ--IIMCLLNKHLFFSPELSAVQTRTTGRSLWVC-----VSSISTGEI 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DRGPKPLNIIYKVVNJGLKGLPVSVTLSLPCQ------TTHVTLTPHNPSMQ 974
                                                                                                                                                                                                                                                820 SKFDAIKPSRTR-----SSCGDRDSGAINRITCSINLPVYRSGTITUFFLGFRVTKW 871
                                                                                                                                                                                                                                                                                                                 DSKASLGNKLILKANVTSENNMPRINKTEFQLELPVKYAVYMVVTSHGV-STKYLNFTAS 929
                                                                                                                                                        NC-NSNSCVADLKLNPSFTN-DTLVVBNQAHFTVLVSLANPGDDSYNTSIVLHYPEGLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1027 FRSSV--NLMARAVLQNVKEYESKYSFY-BFRRDHVFNIS-AELNFNTSRXNQSTGLKYN
                                                                                                                                                                                                                                                                                                                                             DYDWSDRWEMTITANSDNNGNM---SDMSVRRSIPVQFAVELAISLVAEDSVTYLNFSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSHSDFLAELRKAPVVNC-----SIAVCORIQCDIPFFGIQEE
                                   TLKLQLPNCIBDPVSPIVLRLNFS----LVGTPLSAFGNLRPVLAEDAQRLFTALFPFEK
                                                              NCGNDNICODDLSITFSFMSLDCLVVGGPRBFNVTVTVRNDGBDSYRTQVTFFFPLDLSY
                                                                                                                                                                                                                    814 RKVSTLONORSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 23, Last an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Thumbikat P., Kannan M.S., Maheswaran S.K.;
"Sequence of the alpha subunit of bovine lymphocyte function-
associated antigen 1.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440778; AAN63636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.5%; Score 1264; DB 6; Length 9 
llarity 34.7%; Pred. No. 1.1e-84; 
Conservative 165; Mismatches 388; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, A32039, A32039.

PIR, A32039, A32039, A32039, A32039, A32039, A32039, Cintegrin complex; IEA, G0:00069305, Cintegrin adhesion receptor activity; IEA. G0; G0:0004895, Ficell-matrix adhesion; IEA. InterPro; IPR000413; Integrin_alpha.

InterPro; IPR000413; Integrin_alpha.

Pfam; PF01092; VWA. 1.
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927 AA; 102523 MW; 02E2CF099170B1EC CRC64;
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SMART; SMO0191; Int alpha; 4.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
NON_TER 927 927
SRQÜENCE 927 AA; 102523 MW; 02F2CPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMENARY;
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Best Local Similarity
Matches 339; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEPIRLQVP----VEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLROOPOKFPEALRGCPORDSDIAFLIDGSGSIIPHDFRRNKELVSTIMEOLKKSKTLFS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 SL-QAVSNFTAAYQECSKREVNLVFLFDGSSSMKAVEFDMNKNFIKDVMKKLSNSSIKFA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 IMOYSEEFRIHFTFKEFONNPNPRSLIKPITOLLGRIHTATGLRKVVRELFN-ITNGARK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAFKILFLLTDGEKFGDPLGYED--VIPELDREGVIRYVLGFGDAFRSEKSRQELNTVAS 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 KPPRDHVFQANNFEALKTVQNQLRBKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSTVGSYDWAGGVFLYT -- SKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHY 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YE-OTRG-GOVSVCPLPRGORARWOCDAVLYGEQ--GOPWGRFGAALTVLGDVNGDKLTD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAIGAPGEEDNRGAVYLFHGTSGSGISPSHS-QRIAGSKLSPRLQYFGQSLSGGQDLTMD 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAVGAPLE - - NEGVVYIXLGDGTHGINPEHAPQRIPARSVLPGLQQPGVSLSGQMDMNDD 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 GLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPRBVARNVFECNDQVVKGKEAGEVRVÇLH 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         594 NLPDIVIGTQGGIVLLINARPVMSVSAQLSFNPMBISLNYFECPGS--NAFNAFNLTSCFT 651
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EMBL; AB048537; BAB39135.1; -. EMBL/GenBank/DDBJ databases.

R MSP 202001; ILFA.

GO; GO:0008305; C:integrin complex; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0007160; F:cell adhesion receptor activity; IEA.

R GO; GO:0007160; F:cell-matrix adhesion; IEA.

R InterPro; IRR001969; Aspprotease AS.

InterPro; IRR001969; Aspprotease AS.

InterPro; IRR001919; Integrin_alpha.

R Pfam; PPO0357; integrin_A, i.

R Pfam; PPO0357; integrin_A, i.

R Pfam; PPO0357; integrin_A, i.

R PRINTS; PRO0453; VWFADOWAIN.

R SMART; SW00191; Int alpha; S.

R PROSITE; PS00141; ASP_PROTEASE; I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.6%; Score 1329.5; DB 13; Length 1187 Best Local Similarity 31.0%; Pred. No. 2.3e-89; Matches 369; Conservative 210; Mismatches 456; Indele 157;
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                                              HUVKHIYQVRIQPSNYDNMP-PLEALVRVPRVHSEGLITHKWSIQMEPPVNCSPRNLESP
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 24, Last sequence update)
101-OTN-2003 (TrEMBLrel. 24, Last annotation update)
101-OTN-2003 (TrEMBLrel. 24, Last annotation update)
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Bukaryota; Matazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE-98056820; PubMed-9394838;

A Breman M., Rees D.J.G.;

A Breman M., Rees D.J.G.;

"Sequence analysis of rat integrin alpha B1 and alpha B2 subunitiesure expression reveals phenotypic similarities between tissue and dendritic cells in lymph.";

But. J. Immunol. 27:3070-3079(1997).

EMBL; AP020045; AAC23662.1; -.

EMBL; AP0200485; F:cell adhesion receptor activity; IBA.

GO: GO:0004895; F:cell adhesion receptor activity; IBA.

GO: GO:0004895; F:cell adhesion receptor activity; IBA.

RO: GO:0004895; F:Cell adhesion 
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547
                                                                                                                                                                                                                                                     STBEL----CREDCFSNITIKVTYE-----FQTSGGREDYPNTL--DHYKEPSAIFQLP
                                                                                                                                                                                                                                                                                       FEKNYCHNDNI CODDISITES FMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFPPLD
- EEDAFVRRIEGEQMGSYFGSVLCPVDIDMDGTTDFLLVAAPFYHIRGEEGRVYVYQVPE
                         GORARWOCDAVLYGEGGOPWGRFGAALTVLGDVNGDKLTDVAIGAP-----GEEDNRGA
                                          -QDASFSLAHTLSGHPGLTNSRFGFAMAAVGDINQDKFTDVAIGAPLEGFGAGDGASYGS
                                                                                                                               LRSOPVLRVKAIMEFNPREVARNVFECNDOVVKGKEAGEVRVCLHVQKS---TRDRLREG
                                                                                                                                                       LRSRPVVDLTVSMTFTP-----DALPMVFIGKM--DVNLCFEVDSSVVASEPGLREM
                                                                                                                                                                                                           FINETVDVDV-------TRORORIÓCEDSSGCOSCLRKWNGGSFLCEHFWLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1026 SQEPACGSDPVQHVKEWHSVVCAI------TSNKENVTVAARISVG
                                                                          VYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLL
                                                                                                                                                                                   QIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTC------
                                                                                                                                                                                                                                    ETLKLOLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLR----PVLAEDAORLFTALF--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 24, Last annotation update)
Integrin alpha E2 (Fragment).
Buttus norvegicus (Rat).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Marmalia; Butheria, Rodentia; Sciurognathi; Muridae, MucBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSVGGILLIALITAALYKLGFFKRQYKDYMSE 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSSIGGLLVLVVIIAILFKCGFFKRKYQQLNLE 1152
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                 activity; IEA
GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0004895; F:cell_adhesion receptor activi
GO; GO:0007160; P:cell_adrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000235; WWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00035; wws; L.
PRIWES; PR00185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; INT. alpha; 4.
SWART; SW00131; INT. alpha; 4.
SWART; SW00137; VWF, I.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
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1 SEQUENCE 1167 AA; 128593 WW; E3PED7E18B5CBE
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111 GSNIRQQPQKFPBALRGCPQRDSDIAFLIDGSGSIIPHDFRRMKELVSTIMBQLKK 166	225 ITNGARKNAFKLIFLITDGEKFEDPLGYEDVIPELDREGVIRYVLGFGDAFRSEK 279 256KGGRKGARKVMIVITDGESHDSP-DLEKVIRGSEKDNVTRYAVAVLGYYNRRGINPET 312 280 SRQELNIYASKPPRDHVPQANNFRALKTVQNQLREKFFALFATGTGTGSSSFFHEMSGBF 339	313 FLNEIKYTÄSDPDKHFFNYTDEAALLI IVALGERIFILEGTRIK.ETSFGLEMISQTGF 371 340 SAAITSNOPLLSTVGSYDWAGGVELYTSKEKSTFINMTRVDSDNNDAYLGYAAAI 394 : : :	395 ILRNRV-QSLVLGAPRYQHIGLVAMF-RONTGMWESNANVKGTQIGAYPGASLGSVDVDS 452 :::	453 NGSTDLVLIGAPHYYEQTR-GGOVSVCPLPRGGRARWQCDAVLYGEQGPWGRFGAALTV 511 :	512 igdvingdkijdvalgapgeeddrrgavylfhgtsgsgispshsqriagski.sprloyfggs 571 :	LSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVK	630 GKEAGEVRVCLHVQKSTRDFLREGQIQSVVTYDLALDSGRPHSRAVF 676	677 NETKNS-TRRQTQVLGLIQTCETLKLQLPNCIEDPVSPIVIRLNFSLVGTPLSAFGNLRP 735 :	736 VLABDAQRLFTALPPFEKNCGNDNICQDDLSIT 768 :	769 FSFMSLDCLAVGGPREFNYTVTVRANGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW 828	829 RLACESASSTEVGGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLKANVT 887	888 SENNMPRINKTEPQLELPVKYAVYMVVTSHGVSTKYLMFTASENTSRVMQHQ 939	YQVSNIGQRSLPISLVFLVPV	972 QVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIPFFGIQEEF 1028	1029 NATLKGNLSFDWYIKTSHNHLLIVSTARILFNDSVFTLLPGQGAFVRSQTETKVEPF 1085
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Qy 722 LVGTPLSARGNLRPVLAEDAQRLETALPPPEKNCGNDNICQDDLSITFSFMSLDCLVV 779 Db 782 F-OTSEERRNHPNPILDHYKEPSAIPQLPYEKDCKNKVFCIABIQLTTALSQQD-LVV 837 Qy 780 GGPREFNVTVTVRNDGEDSYRTQVTFPFPLDLSYRKVSTLQNQRSQRSWRLACESASSTE 839 Db 838 GITKEVTMNISLTNSGEDSYMTNMALNYPRNLQFKKIQKPLSPDIQCDDFKPV- 890	QY 840 VSGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTE 899 :: : : :	Db 948SLOFRHAFIAVLSRPSVMYNNTSOSSBHKEFFFNVHGENHFGAVPQLQICVP 1000 Qy 960 VRLNQTVIWDRPQVTPSENLSST-CHTKERLPSHSDFLABLRKAPVNCSIAVCQRIQCD 1018	QY 1019 IPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTL 1066 Db 1040EEWHSVICAITSNKENVTVAAEISMGHTKQLIRDISELQILGEISFNKSLYEG 1092	Qy 1067 LPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQY 1122	Oy 1123 KDMMKB 1128 Db 1147 KQLNLB 1152	RESULT 15 Q7TQC3 ID Q7TQC3 PRELIMINARY; PRT, 1188 AA.	AC Q7TQC3; Df 01-OCT-2003 (TrEMBLrel. 25, Created) Df 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) Df 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	All integrin. ITGAll. Mus musculus (Mouse).		KP SEQUENCE FROM N.A. RA Tiger Tries. Popova S.N., Velling T., Ekman S., Forsberg E., RA Gullberg D., RT "allb1 integrin is important for mesenchimal cell function:		RA Johansson M., Popova S.N.; RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AY124460; AAM62130.1; - KW Intecrin.	SEQUENCE 1188 AA; 133067 MW; 69B2BF20D75E4271 CRC64; Query Match 17.7%; Score 1038.5; DB 11; Length 1188; Sect Local Similarity 28.1%; Pred. No. 1e-67;	; CONSELVATIVE 182; MISMALCRES 495; INCEIS 213; GADS FNLDTENAMTFQ-ENARGEGGSUVQLQGSR-VVVGADQEIVAANQRGSLYQCDYSTGS	5.7 5.7 8.3

us-09-902-481b-3.rspt

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Search completed: June 7, 2004, 17:16:16 Job time: 46.4889 secs

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GenCore version 5.1.6
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Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	June 7, 2004, 16:54:39 ; Search time 49.4608 Seconds (without alignments) 6495.175 Million cell updates/sec	US-09-902-481B-3 e: 5879 1 FNLDTENAMTFQENARGFGQFKRQYXDNMSEGGPPGAEPQ 1137	e: BLOSUM62 Gapop 10.0 , Gapext 0.5
	OM protein -	Run on:	Title: Perfect score: Sequence:	Scoring table:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

1586107

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seg length: 0 Maximum DB seg length: 2000000000

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw65090 Human Bet	Aab07360 Human CD1	Aau80252 Human int	Abg61469 Human Bet	8	Add25615 Binding d	Aar04136 Alpha sub	Aar07120 p150.95 a	$\overline{}$	Aab07361 Human CD1	Abg61470 Human Bet	Abu07406 Protein d	Aar78166 Human bet	Aaw23049 Human bet	Aaw57491 Human bet		Aaw72825 Human alp	2 Human	Aab07359 Human alp	Abg61468 Human Bet	Aaw23064 Human bet	Aaw65106 Human Bet	Aaw72837 Human alp	Aaw73343 Human alp	Aab07376 Human alp
SUMMARIES	JD	AAW65090	AAB07360	AAU80252	ABG61469	AA014428	ADD25615	AAR04136	AAR07120	AAW65091	AAB07361	ABG61470	ABU07406	AAR78166	AAW23049	AAW57491	AAW65089	AAW72825	AAW73342	AAB07359	ABG61468	AAW23064	AAW65105	AAW72837	AAW73343	AAB07376
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d¥	Query Match	99.3	99.3	99.3	99.3	99.3	99.3	99.1	58.5	58.2	58.2	58.2	58.2	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.4	57.4	57,4	57.4	57.4
	Score	5839	5839	5839	5839	5839	5839	5829	3437	3423	3423	3423	3421	3388	3388	3388	3388	3388	3388	3388	3388	3372.5	3372.5	3372.5	3372.5	3372.5
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Abg61485 Human Bet	Aar78169 Rat alpha	Aaw23062 Rat beta	Aaw60004 Rat alpha	Rat	Aab07374 Rat alpha	Abg61483 Rat Beta2	Rat	Aaw73345 Rat alpha	Aaw23061 Mouse bet	Aaw60003 Mouse alp	Mouse	Aaw72836 Mouse alp	Aaw73347 Mouse alp	Aab07373 Mouse alp	Abg61482 Mouse Bet	Aar78168 Mouse alp	Aaw23059 Rat beta	Aaw60001 Rat alpha	Aaw65101 Rat beta-
ABG61485	AAR78169	AAW23062	AAW60004	AAW72824	AAB07374	ABG61483	AAW65104	AAW73345	AAW23061	AAW60003	AAW65103	AAW72836	AAW73347	AAB07373	ABG61482	AAR78168	AAW23059	AAW60001	AAW65101
61 5	61 2	61 2	61 2	61 2	61 3	61 5	61 2	61 2	61 2	61 2	61 2	61 2	61 2	61 3	61 5	61 2	51 2	51 2	51 2
11	116								1161										
57.4	54.7	54.7	54.7	54.7	54.7	54.7	54.5	54.5	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.3	54.3	54.3
3372.5	3215.5	3213.5	3213.5	3213.5	3213.5	3213.5	3206.5	3206.5	3201	3201	3201	3201	3201	3201	3201	3197	3192.5	3192.5	3192.5
56	27	28	29	30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA. (first entry) 28-SEP-1998 AAW65090; AAW65090

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis.

93US-00173497. 94US-00286889. 94US-00362652. 95US-00485618. 23-DEC-1993; 05-AUG-1994; 21-DEC-1994; 07-JUN-1995; Homo sapiens US5728533-A. 17-MAR-1998.

Van Der Vieren M, Gallatin WM; WPI; 1998-206565/18.

(ICOS-) ICOS CORP.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes. Example 5; Fig 1A-D; 106pp; English. This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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AB07360 D AAB07360 standard; protein; 1153

AAB07360;

17-JAN-2001 (first entry)

Human CD11b protein sequence.

Human; macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.

Homo sapiens.

WO200029446-A1

25-MAY-2000.

16-NOV-1999; 99WO-US027139

16-NOV-1998; 98US-00193043.

(ICOS-) ICOS CORI

Gallatin MW, Van Der Vieren M;

WPI; 2000-387751/33.

Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury sites.

Example 5; Fig 1; 270pp; English.

Integring are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte cintegrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha cyproximately 60% identity to the protein sequence of alpha_d. The Alpha_d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple sclerosis, astima, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatorid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the inhibition of macrophage infiltration at the site of a central nervous system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease

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This invention relates to a modified integrin-I or integrin I-like domain to polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or imunosuppressive activities. The invention may have antiinflammatory or imunosuppressive activities. The invention is mannatory or imunosuppressive activities. The invention comparing an integrin appear conformation and are useful as invention, or antibodies that selectively bind to integrin I-C domain; and for identifying a modifiator of integrin activity, or of invention, or antibodies (preferably anti-LRA-I antibody) is useful for treating or preventing an integrin mediated disorder which is an comparing of an integrin to a cognate ligand such as Crohn's disease, nephritis, human immunodeficiency virus (HIV), myocardial infarction, Slorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for composition mediated disorder in a subject. The polypeptides of integrin mediated disorder in a subject. The polypeptides of integrin-mediated disorder in a subject. The polypeptides of integrin-mediated disorder in a subject. The mutant the human cinception.
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                                                                                                                                                                                                                                              1097 KVEPPRVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153
                                                                                                                                                                                          KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                              1037 FFGIQEEFNATLKGNLSFDWYIKTSHWHLLIVSTABILFNDSVFTLLPGQGAFVRSQTET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inffammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; sjorgen's syndrome; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified integrin-I or integrin I-like domain polypeptide useful as immunogen to produce antibodies specific to polypeptide, comprises disulfide bond such that polypeptide is stabilized in a desired conformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human integrin 1 alpha-M subunit protein
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The invention relates to promoting locomotor recovery, inhibiting an accomplot damage, limiting locomotor impairment, or limiting autonomic and sensory defenction following spinal cord injury by administering an anti-alpha d (Betaz integrin alpha2 subumit) monoclonal antibody to a nati-alpha d (Betaz integrin alpha2 subumit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule. The method is useful for promoting impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphab colbws and proteins, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative collits, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha protein sequence RLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIP 1036 Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD; leukcoyte adhetion deficiency; inflammatory response; diabetes; multiple sclerosis, arthitis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM.R; VCAM-1; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; locomotor recovery; locomotor damage; locomotor impairment; autonomic dysfunction; sensory dysfunction; spinal cord injury. Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153 1037 FFGIQEERNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET Human Beta2 integrin alphaCD11b subunit. Example 5; Page 191-194; 270pp; English. ABG61469 standard; protein; 1153 Van Der Vieren M; 15-OCT-2001; 2001WO-US032059 13-OCT-2000; 2000US-00688307. (first entry) WPI; 2002-463260/49. (ICOS-) ICOS CORP. WO200230980-A2. Homo sapiens. Gallatin WM, 27-AUG-2002 18-APR-2002. 1097 ABG61469; 977 1021 1081 RESULT 8 셤 δ 윤

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The invention comprises structurally biased variant integrin inserted (I) domain proteins, wherein the alterations to the protein occur in at least we noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins and nucleic acids encoding the variant integrin I domain proteins.

The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatoid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating ischaemia/ repertusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for the abbanit of integrin
                                                                                                                                                                                                                                                                                                                          Mac-1, integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related immunological disorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
                                                                           KVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKIGFFKRQYKDMMSBGGPPGAEPQ 1137
                                                                                              1097 KVEPFEVPNPLPLIVGSSVGGILLLALITAALYKIGFFKRQYKDWASEGGPPGAEPQ 1153
        New integrin I domain protein having alteration in at least 2 noncontiguous regions and exits in an open conformation, useful for treating, preventing or suppressing inflammatory or immunological disorders.
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Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidabetic; antithyroid; anteroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1, antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-fiscorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaathenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                         Binding domain-immunoglobulin fusion protein-associated protein #85
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                                                                ADD25615 standard; protein; 1153
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RESULT 6
ADD25615
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2001US-0367358P. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P. 25-JUL-2002; 2002US-00207655 (GENE-) GENECRAPT INC. US2003118592-A1. Unidentified, 17-JAN-2001; 26-JUN-2003.

PA Thompson Leabetter JA, Hayden-Leabetter MS, WPI; 2003-801317/75. New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

Disclosure; SEQ ID NO 176; 157pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hasey chain comprising a binding domain polypeptide that is fused to the hinge region contact region polypeptide that is fused to the hinge region polypeptide that is fused to the case to the hinge region polypeptide comprises; a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises; a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more oysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more oysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide contains on cysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues of at least one immunoglobulin hinge region polypeptide contains or oysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues of at least one immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytocoxicity (ADCC) and complement fixation. The binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynuclectide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin immunoglobulin immunoglobulin are expension of a host cell transformed or transfected with a recombinant expression

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pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymulocide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, mysthenia gravis, Grave's disease, type I diabetes mellitus, multiple sollerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence. Late the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

Sequence 1153 AA;

RLOVPVEAVNAMSLGLSLAATTSPPOLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 77 RLÓVPVBÁVNMSLGLSLAATTSPPOLLACGPTVHQTCSBNTYVKGLCFLFGSNLRQQPQK 136 FPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF 180 FPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF 196 RIHFTFKEFQNNPNPRSLIKPITQLLGRIHTATGLRKVVRELFNITNGARKNAFKILFLL 240 | TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN 300 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN 316 NFEALKTVONOLREKI FALBGTOTGSSSSFEHEMSOBGFSAALTSNGPLLSTVGSYDWAG 360 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILENRVQSLVLGAPRYQHIGLVAMFR 436 QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 480 ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 496 540 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 600 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVVGAQGHVLLLRSQ 616 PVLRVKAIMEFNPREVARNVFECNDQVVKGKBAGEVRVCLHVQKSTRDRLREGQIQSVVT 676 720 736 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780 SLVGTPLSAFGNLREVILAEDAQRLFTALFPFEKNCGNDNICQDDLSITPSFMSLDCLVVG 796 PVLRVKAIMEFNPREVARNVFECNDQVVKGKRAGEVRVCLHVQKSTRDRLREGQIQSVVT 660 9 36 FNLDTENAMTEQENARGFGQSVVQLQGSRVVVGAPQBIVAANQRGSLVQCDYSTGSCEPI PRGORARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKL-TDVAIGAPGEBDNRGAVYLP FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF Gaps ö 99.3%; Score 5839; DB 7; Length 1153; 98.9%; Pred. No. 0; ive 8; Mismatches 5; Indels 0 Best Local Similarity 98.9 Matches 1124; Conservative 137 257 317 377 -1 17 617 677 61 121 181 197 241 301 361 421 437 481 497 541 557 601 661 721 737 Query Match ದ್ದ 쉱 đ 셤 ò 유 8 6 6 8 셤 셤 g Ò 쉱 Ś 셤 ò ठे ò d ò ઠે ઠે ò

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ò	901 QLELP	QLELPVKXAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNIAGRSLPISLVFLVPV 960
q	917 QLELP	VKXAVYMVVTSHGVSTKYLNFTASENTSRVÆQHQYQVSKLGQRSLPISLVFLVPV 97.
ò	961 RINOT	RINQIVIMDRPQVIFSENLSSTCHTKERLPSHSDFLARIAKAPVVNCSIAVCQRIQCDIP 102
đ	977 RLNOT	VINDRPQVIPSENLSSTCHTKERLPSHSDFLABLKAPVVNCSIAVCQRIQCDIP 10.
ò	1021 PFGIQ	PGIOBENATIKGNISFDWYIKTSHNHILIVSTABILFNDSVFTLLPGQZAFVRSQTET 10
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ò	1081 KVEPF	KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGSPPGAEPQ 1137
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RINGTVIMDRRQVTFSENLSSTCHTKERLESHSDFLABIRKAPVVNCSIAVCGRIQCDIP 1020
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rhinovirus.
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                  QNICHWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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20. .4
/label= N-terminus
61. .63
/label= glycosylation si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MRR-2003 to correct PR field.) (Updated on 2-MRR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFEALKTIONOLREKIFALEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
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/label= putative N-glycosylation site 1022. . 1024
/label= putative N-glycosylation site 1045. .1047
/label= putative N-glycosylation site 1051. .1053
/label= putative N-glycosylation site 1076. .1078
/label= putative N-glycosylation site 1076. .1078
/label= putative N-glycosylation site 1106. .1134
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Best Local Similarity 98.8%;
Matches 1123; Conservative
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                                                    TDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKELNDIASKPSQEHIFKVB 317
                                                                                                NFBALKTVQNQLREKIPAIBGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360
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     QTHFTFEEFRRTSNPLSLLASVHQLQGFTYTATAIQNVVHRLFHASYGARRDATKILIVI 257
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                                                                                                                                                                                                                                                                                           PRGQRARWQCDAVLYGBQGQPWGR FGAALTVLGDVNGDKLTDVA I GAPGEEDNRGAVYLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of viral esp. rhino-viral infection - by admin. of alpha sub-
unit of p150.95 cell surface adhesion receptor, opt. together with a beta
chain of CD-18 family.
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                                                                        /label= glycosylation site 697. .699
71sbel= glycosylation site 735. 737
71abel= glycosylation site 899. .901
/label= glycosylation site
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89. .91
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385. .387
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/label= transmembrane
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tes 681;
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                                                                                                                                                                                                                                                                                                                                       Screening assay for modulators of integrin binding - using immobilised o: labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
Beta-integrin alpha-d subunit, human, modulator, treatment, psoriasis, type-r diabetes, atherosclerosis, multiple sclerosis, asthma; lung inflammation; acute respiratory distress syndrome, CDlic subunit, rheumatoid archritis.
                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 1A-D; 106pp; English.
                                                                                                                                                                                                                                                                                 Van Der Vieren M, Gallatin WM;
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94US-00362652.
                                                                                                                                                                                            93US-00173497
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                                                                            Homo sapiens
                                                                                                                                                                 07-JUN-1995;
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61 RLOVPVEAVNMSLGISLAATTSPPQLLACGPTVHQTCSBNTYVKGLCFLFGSNLRQQPQK 120
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                                                                                                                                                                 20 FNLDTEELTAFRYDSAGFGDSVVQYANSWVVGAPQKIIAANQIGGLYQCGYSTGACEPI 79
                                                                                                                          1 FNLDTENAMIFOENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                                                               6; Gaps
tch 58.2%; Score 3423; DB 2; Length 1163; al Similarity 60.2%; Pred. No. 2.7e-274; 680; Conservative 149; Mismatches 294; Indels 6;
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1020 PFFGIQEEFNATLKGNLSPDWYIKTSHNHLLIVSTARILFNDSVFTLLPGQGAFVRSQTE 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1035 PSFSVQRELDFTLKGNLSFGWVRQILQKKVSVVSVARIIFDTSVYSQLPGQEAFWRAQII 1094
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                                                                                                          438 QVSRQWRMKABVIGTQIGSYFGASLCSVDVDTDGSTDLVLIGAPHYYBQTRGGQVSVCPL
                                                                                                                                                                                                                                                                                       677 IDIALAPGRISPRAIFQETKURSLSRVRVIGLKAHCENFNLLLESCVEDSVIPIILRINF
                                                                         QNTGMWESNANVKGTQ1GAYFGASLCSVDVDSNGSTDLVL1GAPHYYEQTRGGQVSVCPL
                                                                                                                                                                     PRGORARWOCDAVLYGEOGOPWGRFGAALIVIGDVNGDKLIDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                           541 KGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSO
                                                                                                                                                                                                                                                                                                                                                       PVLRVKAIMBFNPREVARNVFBCNDQVVKGKEAGEVRVCLHVQKSTRDRLREGOIQSVVT
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AAB07361 standard; protein; 1163 AA
                                   Human CD11c protein sequence.
                           (first entry)
                          17-JAN-2001
                  AAB07361;
RESULT 10
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Human, macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11c.

Homo sapiens.

WO200029446-A1

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(first entry)
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                                                                                                                                                                                                                                               in cellular adhesion. Integrine are made up of an alpha subunit and a in cellular adhesion. Integrine are made up of an alpha subunit and a beta subunit. One class of human integring are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit cDlic. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit: alpha d (AAMS0014 and AAB07359). The present sequence has subunit: alpha d (AAMS0014) in the response of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosalerosis, multiple celerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease
                                                                                                                                                             Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFEALKTVONOLREKIFAIEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360
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Pred. No. 2.7e-274;
                                                                                                                                                                                                               Example 5; Fig 1; 270pp; English.
                                                                                                               Van Der Vieren M;
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60.2%;
                          99WO-US027139
                                                 98US-00193043
99US-00350259
                                                                                                                                     WPI; 2000-387751/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1163 AA;
                                                                                     SODI (-SODI)
                                                                                                             Gallatin MW,
                         16-NOV-1999;
                                                16-NOV-1998;
08-JUL-1999;
 25-MAY-2000
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QVSRQWRMKAEVIGROIGSYPGASLCSVDVDTDGSTDLVLIGAPHYYRQTRGGQVSVCPL
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                                                                                                              PRGWR-RWWCDAVLYGEOGHPWGRFGAALTVLGDVWGDKLTDVVIGAPGEERRGAVYLF
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138 QVSRQWRMKAEVIGTQIGSYFGASLCSVDVDTDGSTDLVLIGAPHYYEQTRGGQVSVCPL 497
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                                                                                                                                                                                                                                                                 The invention relates to promoting locomotor recovery, inhibiting commotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrins contemplicated in diseases such as IAM (leukocyte adhesion deficiency, are implicated in diseases such as IAM) (leukocyte adhesion deficiency, are implicated in diseases such as IAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory response, diabotes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, inmune complex alveolitis and leukaemia. The present sequence is Beta2 integrin alpha subunit sequence included for comparison with the Beta2 integrin alphaD protein sequence
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                                                                                                                                                                    Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.
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   15-OCT-2001; 2001WO-US032059.
                                  2000US-00688307
                                                                                                     Van Der
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                                  13-OCT-2000;
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                                                                                                   Sallatin WM,
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                                                                    HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
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                                                                                                                                                             617 PVLWVGVSMOPIPARIPRSAFECREOVVSEQTLVOSNICLYIDXRSKNLLGSRDLQSSVT
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                  498 PRGWR-RWWCDAVLYGBQGHPWGRRGAALTVLGDVWGDKLTDVVIGAPGBEENRGAVYEP
                                                                                                                                                                                                                                                                                                                                                         GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGBBDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 TKVEPPBVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein differentially regulated in prostate cancer #9.
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The invention describes genes (1) which are differentially regulated in prostate cancer. (2) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (2) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate cancer of target genes which are differentially-regulated in prostate cancer colls, which involves contacting a polypeptide differentially-regulated in prostate cancer calls with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (1) is useful as molecular markers, as exput sargets, and for detecting, is useful as molecular markers, as full transfers, and for detecting, prognosting, stading, grading, predistoring, prognosticating, prognosticating, products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (1) and its expression products are used in the diagnostic test to assay for presence of cancer, its stage of development, the nature of genetic defect, etc. The modulate propression problems as target for therapy or drug of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide and thus so in the polypeptide and thus to incondent permit polypeptide and thus conditions are used in the diagnosic cancer of the polypeptide and thus of specific genes, and groups of genes, expressed in pathways which are useful in diagnosit, therapeutic, and clinically relating the propresed cancer. The identific
                                                                                                                                Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                         Claim 1; Page 225-228; 416pp; English
                                                                               WPI; 2003-058520/05.
                               Jay
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Sequence 1163 AA;

180 197 240 257 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN 300 9 79 20 FNLDTEELTAFRVDSAGFGDSVVQYANSWVVGADQXITAAANQTGGLYQCGYSTGACEPI RIHPTPKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKBLVSTIMEQLKKSKTLFSLMQYSEEF 138 LPVSRQECPRQEQDIVFLIDGSGSISSRNFATWANFVRAVISQFQRPSTQFSLMQFSNKF FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI .. Query Match 58.2%; Score 3421; DB 6; Length 1163; Best Local Similarity 60.1%; Pred. No. 3.9e-274; Matches 679; Conservative 141; Mismatches 303; Indels 6 121 241 19 181 ద g ò 셤 8 名 ઠે ਨੇ 용

1079 540 780 377 420 437 480 497 600 616 676 720 796 854 959 974 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF 915 QLELPVKYAVYTVVSSHEQFTKYLNPSESEEKESHVAMRRYQVRNLGQRDLPVSINFWVP 378 GAPLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQSLVLGAPRYQHTGKAVIFT PRGWR-RWWCDAVLYGEQGHPWGRRGAALTVLGDVNGDKLTDVVLGAPGEEENRGAVYLF HGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLVVDLAVGARGQVLLLRTR VRINGTVIWDRPQVTPSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI PPFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTE 1035 PSFSVQEELDFTLKGNLSFGWVRQILQKKVSVVSVABITFDTSVYSQLPGQEAFWRAQTT GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR QNTGMWESNANVKGTQ1GAYFGASLCSVDVDSNGSTDLVL1GAPHYYEQTRGGQVSVCPL HGTSGSGISPSHSQRIAGSKLSPRLQYPGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTBV 797 SNLELMAEVMVWNDGEDSÝGTTITFSHPAGLSÝRYVAEGOKÓGOLRSLHLTCDSAPVG--SGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENMPRTNKTEF QLELPVXXAVYMVTSHGVSTXYLNFTAS-BNTSRVMQHQYQVSNLGQRSLPISLVFLVP TKVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKROYKOMMSE 1128 1095 TVLEKYKVHNPTPLIVGSSIGGILLIALITAVLYKVGFFKRQYKEMMEB 1143 498 557 617 855 318 421 438 481 541 601 721 841 901 096 1080 781 음 ઠે 8 셤 δ 셤 ò a ኞ g ⋩ 8 ò g Š g Š 쉱 à g 셤 윱 ઠે 셤 ð Š

Beta-2 integrin alpha-d subunit; antiinflammatory; arteriosclerosis; AAR78166 standard; protein; 1161 AA Human beta-2 integrin alpha-d. (first entry) 28-DEC-1995 AAR78166; RESULT THE SEE SEE SEE E

Location/Qualifiers 17. .1108 Bapiens Key Domain Ношо

301 NFBALKTVQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360

bowel disease; asthma.

inflammatory

480

540

600 615 660 673 720

733

840 852 900

793

Tue

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Beta 2 integrin alpha d subunit; human; cell migration; cell adhesion; phagocytosis; diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; lung inflammation; acute respiratory distress syndrome; rheumatoid arthritis.
                                  PRGORARWOCDAVLYGEQGQPWGRFGAALTVLGDVNGDXLTDVALGAPGEEDNRGAVYLF
                                                                                                                                                                                       HGTSGSGISPSHSQRIAGSKLSPRLQYPGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                                                                                                                                                                                                       YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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              GVFLYTSKEKSTPINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                         I (insertion) domain
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/label= Transmembrane domain
/note= "homologous to the human CD11c transmembrane

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I Similarity 58.9%; Pred. No. 2.2e-271;
665; Conservative 168; Mismatches 288;
                                                    /note= "region homologous to the common to CD11a, CD11b and CD11c
  /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridoma 199M and antibody secreted by it integrin subunit, useful to detect subunit activity.
                                                                                                                                                                                                           1129. .1161
/label= Cytoplasmic_domain
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                              150. .352
/note= "re
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1129. .11
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N-PSDB; AAT79220.
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This represents a human beta2 integrin alpha subunit (alpha d)

polymeptide. This is used in the methods of the invention for isolating a polymeptide encoding a protein that binds to alpha d. The method comprises transforming or transfecting host calls with a DNA construct comprises transforming or transfecting host calls with a DNA construct transcription factor having a DNA-binding domain and an activating transcription factor having a DNA-binding domain or at least part of alpha d and either the DNA-binding domain or the activating domain of the transcription factor and a library of hybrid DNA sequences encoding fusions of at least part of putative alpha d-binding proteins and the DNA-binding domain or the activating domain of the transcription factor which is not incorporated in the first fusion are expressed in the host cells. The binding of an alpha d-binding protein to alpha d in a particular host cell is detected by determining production of the reporter gene product in the cell. The hybrid DNA sequence encoding the reporter gene product in the cell. The hybrid DNA sequence encoding the reporter gene product in the cell. The hybrid DNA sequence encoding the reporter gene product in the cell. The hybrid DNA sequence encoding the reporter gene product in the cell. The hybrid DNA sequence encoding the useful for treating graft arteriosclerosis, alberosclerosis, diabetes, inflammatory bowel disease, arthritis and multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolation of DNA encoding protein that binds to integrin subunit - using recombinant cells containing reporter-transactivator construct.
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Best Local Similarity 58.9%; Pred. No. 2.2e-271;
Matches 665; Conservative 168; Mismatches 288;
                                                                                "extracellular domain"
                                                                                              domain"
                                  17. .1161
/note= "mature protein"
                "signal peptide"
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94US-00286889.
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N-PSDB; AAV31540.
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05-AUG-1994;
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Patent No. 5437958

GENERAL INPORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
ITILE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSERE Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 111inois
COUNTRY: USA
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ITILE OF LOGG-6402
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                                   US-08-482-293A-2
US-08-943-363-2
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98.9%; Pred. No. 0;
live 8; Mismatches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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STRANDEDNESS: sir
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Matches 1124; Conserv
 TOPOLOGY:
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US-08-173-497-3
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PcTUG_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-286-889-3
US-08-485-618-3
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US-08-655-672-3
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US-08-285-618-4

US-08-865-618-4

US-08-605-672-4

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Maximum Match 100%
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ZIP: United States

ZIP: 60606-6403

CONTRY: United States

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CONTRY: Whited States

CONTRY: Whited States

CONTRY: Whited States

CONTRY: No. Compatible

CONTRY: READABLE FORM:

MEDIUM TYPE: POC.DOS/MS-DOS

SOFTWARE: PAPELCATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/286,889

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99.3%; Score 5839; D
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1124; Conservative 8; Mismatches
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REGISTRATION NUMBER: P38,659
REPERENCE/DOCKET NUMBER: 27866/32168
TELEPOWINICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                          Sequence 3, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      977 RINQTVIMDRPQVIFSENLSSICHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1036
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                        RIÇVPVEAVNMSLGISLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136
                                                                                                                                                                                                                                                                                                         TIGERKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSROBIMTIASKPRDHVFQVN 316
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                                                                                                                                                                                                              NFBALKTVQNQLREKIPAIEGTQTGSSSSPBHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGAWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLF 540
                                                                                                                                                                                                                                                                              TOGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVPQAN 300
                                                                                                                                                                                                                                                                                                                                                                                                   GVFLYTSKEKSTFINNTRVDSDMNDAYLGYAAAIILLRNRVQSLVLGAPRYQHIGLVAMFR 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNTGMMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQ1QSVVT 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDLALDSGRPHSRAVFNETKNSTRROTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDLALDSGRPHSRAVFNBTRXSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSP1VLRLNF 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPREFNVTVTVRNDGEDSYRTQVTFFFFLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPREFNVIVIVRNDGEDSYRTQVIFFFFIDLSYRKVSTLQNQRSQRSWRLACESASSTEV 856
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                                                                                                                       137 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF
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197 RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION NDATA:
APPLICATION NDATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-40G-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 1-DEC-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 11-DEC-1994
ATTORNEY/AGENT INPORMATION:
FELLING DATE: 11-DEC-1994
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION NUMBER: 27866/32797
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312-474-6300
TELEFRAX: 312-474-6448
TELEFRAX: 312-47-6448
TELERY: 312-47-6448
TELERY: 312-47-6448
TELERY: 1153 amino acids
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Best Local Similarity 98.9'
Matches 1124; Conservative
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TOPOLOGY: linear
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MOLECULE TYPE: protein
US-08-485-618-3
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                                   GVFLYTSKEKSTPINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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Fatent No. 5728533
GENERAL INFORMATION:
MAPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. S72853361 Humar. 2 Integrin Alpha Sul
NUMBER OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCES: 103
CORRESPONDENCES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
COUNTRY: United States
COUNTRY: United States
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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99.3%; Score 5839; E
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1124; Conservative 8; Mismatches
                     REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMUNICATION INFORMATION:
TELERPHONE: 312-474-6300
TELERPAX: 312-474-0448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
     REGISTRATION NUMBER: 38,659
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TOPOLOGY: lin
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                                                                          PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 660
                                                                                                    PULRVKAIMEFNPREVARNVFECNDOVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 676
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
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                                                                                                                                                                                                                                                    KVEPFEVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQYKDMASEGGPPGAEPQ 1137
                             SGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRINKTEP
                                           SGALKSTSCSINHPIPPENSEVIFNITFDUDSKASLGNKLLLKANVTSENNMPRINKTEF
797 GPREPNVTVTVRNDGEDSYRTQVTFFFELDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                                                                                   QLELPVXYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
NUMBERS OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STREET: 111inois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/605,672 CLACATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERRNCE/DOCKET NUMBER: 27866/32684
TELECHMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-605-672-3
US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein

US-08-605-672-3
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STRANDEDNESS: sir
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                                                                  FNLDTENAMTFOENARGFGGSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                                                                                                                                                77 RLOVPVEAVNMSLGISLAATTSPPQILACGPTVHQTCSENTYVKGLCFLFGSNLRQOPQK
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                                    Gaps
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Length 1153;
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   DB 2;
 99.3%; Score 5839; E
98.9%; Pred. No. 0;
ive 8; Mismatches
                      Best Local Similarity 98.9
Matches 1124; Conservative
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1021 FPGIQESFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGGGAFVRSQTET 1080
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RIHFTFKEFONNPNPRSLIKFITQLLGRTHTATGLRKVVRELPNITNGARKNAFKILFLL
                                                                  197 RIHFTPKEPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKVAFKLLVVI
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US-08-943-363-3
i. Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
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1037 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLFGGGAFVRSGTET 1096
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                                                                       KVBPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
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                                                                                                                                                                                                                                                                                                             CORRESTONDER ADDRESS

CONTRESSOR ADDRESS

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chloago

STATE: 11linois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,293A
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                                                                                                                                                                                Sequence 3, Application US/08482293A, Patent No. 5831029, GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5831029e1 Human NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
PRIOR APPLICATION DATE:
FILING DATE: 23-DEC-1993
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATE: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams JT. 308-659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFALS 312-474-6300
TELEFALS 312-474-648
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
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TOPOLOGY: lin
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US-08-482-293A-3
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                                                                                    QNIGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYBQTRGGQVSVCPL
                                                                                                      PRGORARWOCDAVLYGEOGOPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Monica
ITILE OF INVENTION: No. 62513951 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT PILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
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US-09-193-043-3
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                                                                                      3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                      ADDRESSES: Marshall, O'Toole, Gerstein, Murray & B
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: 111inois
CONTRY: United States
ZIP: 6606-6402
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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98.9%; Pred. No. 0;
:ive 8; Mismatches
                                                                                                                                                                                                                                                                                                             FILING DATE:
RIGHORALDAN NUMBER: US/08/745/303
FILING DATE:
RPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
ATTONNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
RETERECOMMUNICATION INFORMATION:
TELEBECOMMUNICATION INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITE OF INVENTION: NO. 5837478el Human
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.9
Matches 1124; Conservative
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STRANDEDNESS: sir
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Fatent No. 6432404

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TILE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646

CURRENT PAPLICATION NUMBER: US/09/688,307A

CURRENT PILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: 09/193,043

PRIOR APPLICATION NUMBER: 09/193,043

PRIOR APPLICATION NUMBER: 09/605,672

PRIOR APPLICATION NUMBER: 08/605,672

PRIOR PILING DATE: 1996-02-22

PRIOR PILING DATE: 1994-03-05

PRIOR PILING DATE: 1994-08-05

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1997-10-03

NUMBER: OF SEQ ID NOS: 114

SOFFWARE: PATENTIN VONER: 1897-10-03

NUMBER: PATENTING DATE: 1997-10-03

SEQ ID NOS: 114
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Pred. No. 0;
8; Mismatches
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Best Local Similarity 98.9
Matches 1124; Conservative
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US-09-688-307A-3
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Best Local Similarity 98.9
Matches 1124; Conservative
         NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                         LENGTH: 1153
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Pred. No. 0;
8; Mismatches
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 1153
                                                                                                                                      Query Match
Best Local Similarity 98.9%;
Matches 1124; Conservative
                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
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Sequence 3, Application US/09350259

Patent No. 6620915

GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

APPLICANT: Van der Vieren, Monica

FILLE REPERBNCE: 27866/35004

CURRENT APPLICATION NUMBER: US/09/350,259

CURRENT APPLICATION NUMBER: 09/193,043

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EARLIER FILING DATE: 1993-12-23

EARLIER FILING DATE: 1993-12-23

EARLIER PILING DATE: 1993-12-23

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER PILING DATE: 1993-12-23

EARLIER PILING DATE: 1993-16-65

EARLIER PILING DATE: 1994-08-05
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NKT FLV	917 QLELPVKYAVYMVYTSHGVSTKYINFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV	OY 961 RINOTVINDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVYNCSIAVCQRIQCDIP 1020 Db 977 RINQTVIWDRPQVTPSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1036	OY 1021 FEGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGGGAFVRSGTET 1080 [1081 KVEPFEVPNPLPLIVGSSVGGLILLAALITAALYKUGFFKRQVKDMMSEGGPPGABPQ 113	PFBVPNPLPLIVGSSVGGLLILALITAALYKLGPFKRQYKDMMSEGGPPGAB	RESULT 11 US-08-476-062A-43 ; Sequence 43, Application US/08476062A ; Patent No. 5877275	GENERAL INFORMATION: APPLICANT: Armsout, M. Amin ITLE OF INVENTION: CONTROLLING CELLULAR INMUNE/INFLAMMATORY ITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS) NUMBER OF SEQUENCES: 53) CORRESPONDENCE ADDRESS:) ADDRESSE: Fish & Richardson P.C. ; STREET: 225 Frankin Street	; CITY: Boston ; STATE: MA ; COUNTRY: US ; ZIP: 02110-2804		SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,062A FILING DATE: 07-UNN-1995	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/216,081 ; FILLO DATE: 21-MAR-1994 ; APPLICATION NUMBER: 07/637,830	; FILING DATE: 04-JAN-1991 ; APPLICATION NUMBER: 07/539,842 ; FILING DATE: 18-JUN-1990 ; APPLICATION NUMBER: 07/212,573	FILING DATE: 28-JUN-1988 ; ATTORNEY/AGENT INFORMATION: ; NAME: Freeman, John W. ; REGISTRATION NUMBER: 29,066	шъсф	TELEX: 200154 ; INFORMATION FOR SEQ 1D NO: 43: ; SEQUENCE CHARACTERISTICS: ; LEWOTH: 1152 amino acide	B M	a o

615 999

480 496 540 555

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735 780 795 840 855

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961 RINOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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1096 KVEPPEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDAMASEGGPPGAEPQ 1152
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                                          437 QNTGAMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                                                                                                                            556 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLRSQ
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                                                                                                                                                               PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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                   GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                                            ONTGMMESNANVKGTOIGAYFCASLCSVDVDSNGSTDLVLIGAPHYYEQTR
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PACENT NO. 5424399

PAPLICANT: ARNAOUT, M. AMIN

TITLE OF INVENTION: HUMAN CR3a/D HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

PILING DATE: 16-JUN-1993

PRICH APPLICATION NUMBER: 539,842

PILING DATE: 18-JUN-1990

APPLICATION NUMBER: 539,842

FILING DATE: 18-JUN-1990

APPLICATION NUMBER: 212,573

FILING DATE: 28-JUN-1988

SEQ ID NO:2:
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KVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKOMMSGGPPGABPQ 1152
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                                                                                                                                                                 IDENTIFYING INTEGRIN
                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRAR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 30-JAN-95
ATTORNEY/ACENT INFORMATION:
NAME: JOHN W. FFREMBIN
NAME: JOHN W. FFREMBIN
NAME: JOHN W. FFREMBIN
NAME: JOHN W. FFREMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 5808.5;
Pred. No. 0;
8; Mismatches
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REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUTCATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                     Sequence 43, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: W Amin Arnaout
TITLE OF INVENTION: WITHOUS FOR IDENT:
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
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Best Local Similarity 98.6%;
Matches 1121; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1152
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PCT-US96-01314-43
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PCT-US96-01314-43
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                                             20 FNIDTEELTAFRVDSAGFGDSVVQYANSWVVGAPQKITAANQFGGLYQCGFSTGACEPI
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                                                                                                                                                                                                                                     TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
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Best Local Similarity 60.5%; Pred. No. 4.4e-278;
Matches 683; Conservative 143; Mismatches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPARE: IBM Compatible
COMPARE: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPATER: IBM COMPATE: IBM COMPATER: IBM COMP
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                                                                                                                                                                                                              Sequence 44, Application US/08476062A; Patent No. 5877275 GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
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RECISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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8; Mismatches
  98.68;
Best Local Similarity 98.6
Matches 1121; Conservative
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ZIP: 02110-2804
COMPUTER READALLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model SOZ or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: PCT/US96/01314
FILING DATE: 30-JAM-96
PRIOR APPLICATION DATA: PCT/US96/01314
FILING DATE: 30-JAM-96
APPLICATION NUMBER: 29,066
FILING DATE: 30-JAM-95
ATTORNEY/AGENT INFORMATION:
RECTEMENTATION NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE (617) 542-5070
   ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                    TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
PCT-US96-01314-44
                                Boston
                   STREET: CITY: BOR STATE: ME COUNTRY:
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OTHETERSFRETSNDISLIASVHQLQGFTYTATAIQNVVHRLFHASYGARDATKILIVI 257
                                                                  GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAAPRYQHIGLVAMFR 420
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61 RIQVPVEAVAMSIGLSIAATTSPPQLIACGPTVHQTCSENTYVKGLCFLFGSNIRQQPQK 120
                                                                                                                                                                                                                                                           181 RIHFTFKEFONNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240
                                                                                                                                                                                                                                                                                                                                    121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF 180
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                                                                                                                                               20 FNLDTBELTAFRVDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLYQCGYSTGACEPI
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9
Query Match 58.6%; Score 3446; DB 5; Length 1
Best Local Similarity 60.5%; Pred. No. 4.4e-278;
Matches 683; Conservative 143; Mismatches 297; Indels
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PCT-US96-01314-44

Sequence 44, Application PC/TUS9601314

SEQUENCE 44, Application PC/TUS9601314

SEQUENCE 44, Application PC/TUS9601314

SEQUENCE 44, Application PC/TUS9601314

TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN TITLE OF INVENTION: MATAGONISTS

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:
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1020 PFFGIQEEFNATLKGNLSPDWYIKTSHNHLLIVSTABILFNDSVFTILFGGGAFVRSQTB 1079
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                                                                                                            781 GPREPNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840
                                                                                                                    797 SNLELNAEVAVWNDGEDSYGTTITFSHPAGLSYRYVAGGQQQLRSLHLTCDSAFVG-- 854
                                                                                                                                       SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF 900
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                           PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 660
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Search completed: June 7, 2004, 17:19:19 Job time : 21.3484 secs

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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using sw model - protein search, OM protein

(without alignments) 7512.163 Million cell updates/sec 7, 2004, 17:05:16 ; Search time 14.559 Seconds June Run on:

US-09-902-481B-4 5884 Perfect score: Title:

1 FNLDTENAMTRQENARGFGQ.....FKRQYKDMMSEGGPPGAEPQ 1137 Seguence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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SUMMARIES	D	RWHULB	S00551	RWHU1C	803308	156126	A53213	4,	145914	S44142	A35854	A33998	A41131	S06046	158409	T31437	JC7294	A35761	155534	844250	A36108	T10050	A38457	A27079	B36429	A40021	A27421	iń	1651	31
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ALIGNMENTS

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RESULT 1

KWHU1B

cell surface glycoprotein CD11b precursor [validated] - human

NjAleznate names: complement receptor type 3 alpha chain; leukocyte adhesion protein M

eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

c;Species: Homo sapiens (man)

C;Becies: 31-Dec-1992 #text_change 31-Dec-2000

C;Accession: AJ1108; A28915; A41600; A30892; A32218; A46526; A26091; I52567

S;Corbi, A.L.; Rishimcov, T.K.; Miller, L.J.; Springer, T.A.

J. Bioll, Chem. 263, 12403-12411, 1988

A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, C

A;Reference number: A31108; MUID:88315033; PMID:2457584
A;Accession: A31108
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A;Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Anaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
B;Armaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
Call Biol. 106, 215-2159, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor IA;Reference number: A28915, MUID:88257215; PMID:2454931
A;Accession: A28915
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A;Cross-references: GB:M76724; NID:g180018; PIDN:AAAS8410.1; PID:g553215
R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. US.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhes A;Reference number: A94193; MUID:88190151; PMID:2833753

A; Accession: A30892
A; Molecule type: mRNA
A; Residues: 917-1042 <AR2>
A; Cross-references: GB M18044
R; Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A; Title: cDNA sequence for the alphan subunit of the human neutrophil adherence receptor A; Reference number: A32218; MJD:89098893; PMID:2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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chain reveals homology with the
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1097 KVEPFEVPNPLPLIVGSSVGGILLLALITAALYKLGFFKRQXKDMMSEGGPPGAEPQ 1153
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C;Accession: $00551; 159078

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                               PRGORARMOCDAVLYGEOGOPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: IS9078, MUID:86287312; PMID:2942940
A;Accession: IS9078
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al Similarity 73.8%; Pred. No. 6e-304;
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NAlternate names: leukocyte adhesion receptor p150,95 alpha chain

Call surface glycoprotein CD11c precursor - human

NyAlternate names: leukocyte adhesion receptor p150,95 alpha chain

C;bacession: A36584, A35543; 500864

R;cocssion: A36584, A35543; 500864

R;corbi, A.L.; Garcia-Aquilar, J; Springer, T.A.

J. Biol. Chem. 265, 12750-12751, 1990

A;Reference number: A36584

A;Rocastion: A36583

A;Rocastion: A3684

A;Rocastion: A3684

A;Rocastion: A3684

A;Rocastion: S00864

A;Rocastion: S
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRL-ACESASSTE
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Length 1163;
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 59.0%; Score 3469; DB 1;
llarity 60.9%; Pred. No. 1.8e-234;
Conservative 142; Mismatches 293;
           Similarity
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cell surface glycoprotein CD11a precursor - human
NyAlternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte functio CiSpecies: Homo sapiens (man)
CjDate: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 20-Aug-1999
CjAccession: 803308; A47458; A47555; A48759; 836044
Rilarson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A.Pitle: Primary structure of the leukocyte function-associated molecule-1 alpha subuni
A.Feference number: 803308; MUID:89139587; PMID:2537322
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A)Cross references: GDB:119757; OMIM:153370
A)Map position: 16511.2-16p11.
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom C;Superfamily: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tr C;Foymani: signal sequence #feratus predicted cSIG-7.
F;1-25/Domain: signal sequence #feratus predicted cSIG-7.
F;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted F;154-117/Domain: von Willebrand factor type A repeat homology cVWA2>
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C;Genetics:
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A,Molecule type: mRNA
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Cross-references: EMBL:Y00796, NID:g31421; PIDN:CRA68747.1; PID:g31422
A,Note: part of this sequence was confirmed by protein sequencing
A,Note: part of this sequence was confirmed by protein sequencing
Proc. Natl Acad. Sci. U.S.A. 90, 4221-4225, 1993
A,Title: Deacription of the leukocyte function-associated antigen 1 (LFA-A,Reference number: A47458, MUD:93248261; PMID:8097887
A,Reference number: A47458
A,Residues: 1-20 <COR>
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26.2%; Score 1543.5; DB 2; Length 1170;
Best Local Similarity 34.3%; Pred. No. 1.8e-99;
Matches 403; Conservative 210; Mismatches 460; Indels 101;
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A;Molecule type: DNA
A;Residues: 1-20 <NUE>
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                                             |:||:||:|||| | ::|||| | KVLIIITDGE--ATDSGNIDAAKD----IIRYIIGIGKHFQTKESQETLHKFASKPASE 309
                                                                    HVFQINNFEALKTIQNOLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVG 354
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IS6126 lymphocyte fuction-associated molecule-1-alpha - mouse

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A repeat hom
C;Species: Mus musculus (house mouse)
C;Date: 26-ul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C;Date: 26-ul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C;Accession: 156126
R;Kaufmann, Y: Teeng, E.; Springer, T.A.
A; Immunol. 147, 369-344, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit
A;Reference number: 156126
A;Accession:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               767
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ò	768 TPSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQN 821	Db 295 SSHGSRRKASKN	SSHGSRRKASKVMVVLTDGSIFEDPLNLTTVINSPKWQGVERFAIGVGEEFKSARTAREL 354
qu	:	Qy 285 NTVASKPPRDH	NIVASKPPRDHVFQINNFEALKTIONQLAEKIFAIBGTQTGSSSSFEHEMSQEGFSAAIT 344
õ	822 ORSORSWRLACESASSTRVSGAL-KSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKL 880	Db 355 NLIASDPDETHA	GTVGDALH
qc	832PHSRMPVSCEELTEGSSLLTKTLKCNVSSPIFKAGQEVSLQVMFNTLLNSSWEDFV 887	Qy 345 SNGP-LLSTVGS	SNGP-LLSTVGSYDWAGGVELY-TSKEKSTPINMTRVDSDWNDAYLGYAAAIILRN 398
ò	881 LIKANVISEN-UMPRINKIEFQLELPVKYAVYMVVISHGVSTKYLMFIASENISKVMQHQ 939	Db 412 DBRQVLLGAVG	
셤	888 ELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTQQVQHV 947	Oy 399 RVQSLVLGAPRY	RVOSIVIGAPRYQHIGIVAMPR-QNTGMWESNAMV-KGTQIGAYFGASLCSVDVDSNGST 456
ò	940 YQVSNLGQRSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKE-RLP 990	Db 472 CSLSYVAGAPQY	KHHGAVFELOKBGREASFLPVLBGEOMGSYFGSELCPVDIDMDGST 529
qq	948 YQVRIQPSAYDHNMPT-LEALVGVPRPHSEDLITYTWSVQTDPLVTCHSEDLKRP 1001	Oy 457 DLVLIGAPHYYI	
È	991 SHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLL 1050	Db 530 DFLLVAAPFYHY	
qq	1002 SSEAEQPCLPGVQFRCPIVFRWEILIQVTGTVELSKEIKAS-STLS 1046	Oy S17 GDKLTDVALGAP	GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKUSPRLQYFGQ
ò	1051 IVSTABILENDSVFTLLPGGGAFVRSQTBIKVBPFBVPNPLPLIVGSSVGGLLLALITA 1110	Db 589 QDKLTDVAIGA	
gg	1047 LCSSLSVSFNSSKHFHLYGSKA-SEAQVLVKVDLIHEKEMLHVYVLSGIGGLVLLFLI105	571	
ò	1111 ALYKIGPFKRQYKDMM-SEGGPPGAEP 1136	DD 648 SMAGGPDISGD	
qq	1106 ALYKVGFFKRNLKEKMEADGGVPNGSP 1132	Oy 631 KEAGEVRVCLHT	KEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFKETKNSTKRQIQVL 690 : : : : : : : :
RESULT	9	0 0	
A53213 integrin	n alpha-E chain - human	1 to 1	
C;Speci C;Date:	es: Homo sapiens (man) 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001	757	
C, Acces	sion: A53213 S.K.: Cepek, K.L.; Murphy, B.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.	747	
J. Biol		Db 815 FQLPYEKACKN	
A;Refer A;Acces	1: A53213	Qy 807 FPLDLSYRKVS:	PPLDLSYRKVSTLONORSORSWRLACESASSTEVSGALKSTSCSINHPIPPENSBVTFNI 866 :
A;Status: F A;Molecule	s: preliminary ule type: mRNA	r t	
A; Residues: A; Cross-refe	Residues: 1-1179 <sha> Cross-references: GB:L25851; NID:g457244; PID:g457245</sha>	DY 667 IFDUDSNASLOS	
C,Genetics: A,Gene: GDB	ics: GDB:ITGAE	F 000	WINDERFORM STATE OF THE STATE O
A;Cross A;Map p		200	
C, Super F, 199-3	C.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home F:199-371/Domain: von Willebrand factor type A repeat homology <vwa3></vwa3>	486	
Query	Match 19.4%; Score 1140; DB 2; Length 1179;	OY 978 NESSTORINER : :: :: : : : : : :	NESSICHTEKELESBEDFLEABLENALVONGLAVOUGLEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGE
Best Match	Best Local Similarity 28.9%; Pred. No. 3.5e-71; Matches 340; Conservative 214; Mismatches 451; Indels 172; Gaps 39;	1023	aethenbeveth.pgggafvRsotstkvEpfgvPNPL
à	45 GSLYQCDYSTGSCEPI-RLQVPVBAVNMSLGLSLAAATTSPPQLLACGPTVHQ 95	QM	QILGEISFNKSLYEGLANENHRTKITVVFLKDEKYHSL
q	65 GPLHRCSLVQDBILCHPVEHVPIPKGRHRGVTVVRSHHGVLICIQVLVRRPHS 117	Oy 1092 PLIVGSSYGGE	PLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSE 1128
ර් සි	96 TCSENTYVKGLCFLFGSNLRQQPQ	- - -	: :
දු දු	120 KPPRALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQL 164 :: : : : : : : : : : : : :	RESULT 7 A45226 integrin alpha-1 chain -	numan (fragment)
è		C;Species: Homo sapiens (C;Date: 30-Apr-1993 #sequ	C;Species: Homo sapiens (man) C:Date: 3-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003 C:Annassion: Asf204
QQ	235 KCFECNFALVQYGGVIQTEFDLRDSQDVMASLARVQNITQVGSVTXTASAMQHVLDSIFT 294	C, Accession: A13220 R, Briesewitz, R.; Epstein J. Biol. Chem. 268, 2989-	,
ò.	225 ITNGARKNAFKILFILIDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQEL 284 :: : : :::	A,Title: Expression of na A;Reference number: A4522	ive and truncated forms of the human integrin alpha 1 subunit 5; MUID:93155124; PMID:8428973

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                                                                                                                                                                                                                                                                                                                    SORGPSAAITSNGPLLSTVGSYDWAGGVFLYTSKB----KSTF-INMTRVDSDMNDAYL 388
                                                                                                                                                                                                                                                                                                                                                         GYAAAIILRNRVOSL-VLGAPRYQHIGLVAMPRONTGMWESNANVKGTQIGAYFGASLCS 447
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                                                                                                                                                                107 CFLFGSNIRQOPQKPPBALRGCPQBDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMBQLKK
                                                                                                                                                                                                                                          57 CEP-IRLOVPVEA-----VNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGL
                                                                                                                                                                                                                               ----SKTLFSLMQYSEEPRIHFTFKEFQNNPNPRSLIKPITQLLGR-THTATGLRKVV
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                                                                                                             1 PNLDTENAMTFQENARG-PGQSVVQL---QGSRVVVGAPQBIVAANQRGSLYQCDYSTGS
                                                                                            Gaps
                A,Molecule type: mRNA
A,Residues: 1-1151 -4RI>
A,Experimental source: hepatoblastoma cell line HepG2
A,Note: sequence extracted from NCBI backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAI>
         conceptual translation
                                                                       Query Match
Best Local Similarity 27.8%; Pred. No. 6.1e-68;
Matches 345; Conservative 206; Mismatches 487; Indels
        preliminary; not compared with
Accession: A45226
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integrin alpha 2 subunit - bovine (fragment)
[C.Species: Bos primiqenius taurus (cattle)
[C.Species: Bos 19594 #sequence_revision 16-Aug-1996 #text_change 15-Sep-2003
[C.Species: T.S Puzon, W.; Takada, Y.

R.Kamata, T.; Puzon, W.; Takada, Y.

R.Kamata, T.; Puzon, W.; Takada, Y.

A; Fitle: Identification of putative ligand binding sites within the I-domain of integril A; Reference number: A54402; MUID:94193647; PMID:7511592

A; Reference number: A54402; MUID:94193647; PMID:7511592

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-110 exRAN

A; Residues: 1-110 exRAN

A; Cross-references: GB:L25886; NID:9439695; PIDN:AAB59255.1; PID:9439696

P;161-316/Domain: von Willebrand factor type A repeat homology <VWA2>
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| | |:: ::| | |:: ::|:
| EMTISTD---HIKRGTILDCNTCKFATITCMLTSSDISQVNVSLILWKPTFIKSYFSSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| :|| :| ::
195 FTKTQMGLIQYANNPRVVFNLNTFKSKD---EMIKATSQTFQYGGDLTNTFKAIQYARDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIPFFGIQE-------BFN
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                                                                                                                                                                                                                                                                  FOLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN-----LGQRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPRIKLSISPDNMTSNGYPVLYPTGLSS------SENANCRPHIFEDPFSINSGK
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Best Local Similarity 27.4%; Pred. No. 2.4e-66;
Matches 333; Conservative 219; Mismatches 495; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LPISLVP------LVPVRLNQTVIWDRPQVTPSENLSSTCHTKE
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-KGTOLGAVPGASL 445 QRGDQIGSYPGSVL 484	DAVLYGEQQQPWG 503 		EFNPREVARNVF 621	-SGRPHSRAVFN 677	VGTPLSAFGNL 733		T-EVSGALKSTS 848	KTEFQLELPVKY 908 : : DNSVNLKLSLLY 923	SLPISLVFLV 958 : : : TGSVPVSMA 976	RLPSHSDFLAE- 998 : : QTSSSVFKSEN 1030	NHLLIVSTAEL 1057		TAGILLLALVA 1140		e 15-Sep-2003	.; Damjanovich, L.; I	Laminin adhesion but not		PID:9473099 r <vwa2></vwa2>
AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQLGAYFGASL 	CSVDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPLPRGGRARWCDAVLYGEQGQPWG - : : : CAVDVNKOTITDVLLYGAPMYMNDLKKEEGRVYLFTITKG-ILNWHQFLEGPNGLENA	RFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSGRIAGSKL 	SPRLQYFGQSLSGGODLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVF 	ECNDQVVKGKEAGEVRVCLHVQXSTRDRLREGGIQSVVTYDLALDSGRPHSRAVFN : : : :	· 123	REVIAEDAGRIETALFPFEXONCANDNICQDDLSITFSFMSLDCLVVGGPREFNVTV	TVRNDGEDSYRTQVTPPFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTS ::	CSINHPIPPENSEVTENITEDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLELFVKY ::: : ::: :: : CNVGYPALKSKQQVTFTINFDFNLQ-NLQNQASISFRALSESGSENMADNSVNLKLSLLY	AVYMVVTSHGVSTKYLMFTASENTSRVMQHQYQVSNLGQRSLPISLVF :	PVRLNQTVIMDRPQVTFSENLSSTCHTKE	IRKAPVVNCSIAVCQRIQCDIPPFGIQEBFNATLKGNLSFDMYIKTSHNHLLIVSTARI-	-LPGQGAFVRSQTETKVEPFE-VPNPLPLIVGSSVGGLLLLALITA	TIPLIMKPHEKVEVPTGVIVGSVIAGILLILALVA	OM 1125 	se use mouse) toe revision 13-Jan-1995 #text change	S.; Onodera, H.; Wang, anuary 1994	A-2 homologue supports collagen and		<pre>- <bde>: EMBL:Z29987; NID:g473098; PIDN:CAA82877.1; von Willebrand factor type A repeat homology</bde></pre>
392 AAIILRNRVQSLVIA 	446 CSVDVDSNGSTDLVI : : : : 485 CAVDVNKDTITDVLI	504 REGAALTVLGDVNG : : : 542 RFGSAIAALSDINM	562 SPRLQYPGQSLSGG : 601 SSHLOYPGRSLDGY				790 TVRNDGEDSYRTQVTFFFPLDLSY 	0-0	909 AVYMVVTSHGVSTK : : : : 924 DAEIHIT-RSTNIN	959 PVRLNQTVJWDRPQ 	999 TRKAPVVNCSIAVC		1091 TYNPQIYVIEENTVTIP	1111 ALYKLGFFKRQYKDM : 1141 ILWKLGFFKRKYBKM	T 9 protein homolog - mous cies; Wus muschos (hote: 13-Jan-1995, #sequent	C,Accession: S44142 R,Edelman, J.M.; Chan, B.M.; Uniyal, submitted to the EMBL Data Library, J	5 %	A,Status: preliminary A,Molecule type: mRNA	A,Residues: 1-1178 <bde> A,Cross-references: EMBL:Z2: F;169-344/Domain: von Willel</bde>
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906 VKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR------SLPISLV 955
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                                                                                                                                   55 GSCEPIRLO------VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107
                                                                                                                                                       FERGSNIRQOPQ----KEPRAIRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQL 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 AEDAQRIFTALFPFEKONCGNDNICQDDLSI-----TFSFMSLDCLVVGGPREFNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 -LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMBFNPRBVARNVFBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 NDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFNBT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 YNVGLPGAKIPSGPSSEQFGYSVQQLTNPQGNWLLVGSPWSGPPENRMGDVYKCPVDLPT
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                                                                                                                                                                                                                                                                        165 K--KSKTLFSLMQYSEEPRIHFTFKEFQNNPNPRSLIKPITGLLG-RTHTATGLRKVVRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGTQIGAYFGASLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FNLDTENAMTRQ-ENARGEGOSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST
Length 1178;
Match 18.0%; Score 1057; DB 2; cocal Similarity 27.8%; Pred. No. 2.3e-65; s8 340; Conservative 210; Mismatches 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        848
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Db 496 IDIDKDSYTDLLLUGAPMYMGTEKERGGKVYVYAVNGTRPEYGMSLEPIRGTCCSSLKDN 555 492 AVLYGEGGOPWG-RFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLPHGTSGSGISP 556 556 SCTKERKNEPGAARPGTALAVKDLNVDGPNDVVIGAPLEDDHAGAVYIYHG-SGKTIRE 614 615 STSSKRIKHRGAREGAREGAREGAREGALTALTRAGPULLTRAGPVLAVIYHG-SGKTIRE 614 616 STSSKRIKHRGSKLSPRLQYFGGSLSGGDLTMDGLTVDLTVGAGGHVLLLRSQPVLRVRAINE 610 617 STSSKRIKHRGSKLSPRLGYFGGSLSGGDLTMDGLTVDLTVGAGGHVLLLRSQPVLRVRAINE 610 618 AVAQRIPSGGDGKTLKFFGQSIHGENDLMGDGLTDVTIGGLGGAALFWARDVAVKVTNN 674 619 FNRRVANVPECNDQVVKGKBAG-BVRVCLHVQ-KSTRDRLREGQIOGVVTYDLALDS 667 619 FNRRVANVPRCRVEGKBTVCINATWCFHVKLKSKEDSIYBADLQRVYTLDS 727 679 668 GRPHSRAVFNETEGKSTRQTQVLGLTQTCETLXLQLPNGI	D 738 IAQISSEPSGIGERALQRAITYRESS	Biochem, J. 279, 419-425, 1991
000 000	hain precursor - rat norvegicus (Norway rat) 4, \$11243 larged 709-720, 1990 clouing of the rat integrin 1843 RAA 195-720, 1990 clouing of the rat integrin 1843 RAA 195-720, 1990 clouing of the rat integrin 1843 RAA 196-720, 1990 clouing of the rat integrin 197-84, \$Core 1055; arity 27.48, \$Fed. No. 3.2 arity 27.48, \$Fed. No. 3.2	

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murine lymphocyte
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N.Alternate names: integrin alpha-4
N.Alternate names: integrin alpha-4
C.Species: Mus musculus (Louse mouse)
C.Species: Mus musculus (Louse mouse)
C.Accession: A41131; S16742
C.Accession: A41131; S16742
S.Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzmann, B.; Weissman, I.L.
J. Cell Biol. 115, 1149-1158, 1991
A.Title: Cloning and expression of CDNAs for the alpha subunit of the murine lym
A.Title: Cloning and expression of CDNAs for the alpha subunit of the murine lym
A.Feference number: A41131; MUID:92064645; PMID:1840602
A.Factsosion: A41131
A.Status: preliminary
A.Residues: 1-1039 <ARNA
A.Residues: 1-1039 <ARNA
A.Residues: 1-1039 <ARNA
A.Residues: 1-1039 <ARNA
A.Residues: Louse EMBL:X53176; NID:951484; PIDN:CAA37316.1; PID:951485
C.Superfamily: integrin alpha-4 chain
C.Keywords: cytoskeleton; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEBFNATLKGNLSFDWYIKTSHNH 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 LLIVSTABI-LFNDSVFTLLPGQGAFVRSQTBTKVEPFBVPNP-----LP--LIVGSSVG 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092 VQLTABABINTYNPRIYVI------EDNTVTIPLMIMKPDEKAEVPTGVIIGSIIA 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988
                                                                                                                                                                                                                                                                                         738
                                                                                                                                                                                 722 BRCLGKNMVVVQAQSCPEHIIY1QEPS---DVVNSLDLRVDISLENPGTS-----PALE 772
                                                                                                                                                                                                                                                      EDAQRIFTALFPERNCGNDNICQDDLSITF----SFMSLDCLVVGGPREFNVTVTVRND 794
                                                                                                                                                                                                                                                                                                                                                        GEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTSCSINH 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               914 VTSHGVSTKYLNPTASENTSRVMQHQYQVSNLGQR-----SLPISLVFLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- PVRLNOTVIWDRPQVTF-SENLSSTCHTKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FNLDTENAMTFQ-ENARGFGQSVV-QLQGSR--VVVGAPQEIVAAN----QRGSLYQCDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VEAVMMSLGLSLAATTSP-POLLACG---PTVHQ
                                                                                                                                                         681 NSTRRQTQVLGLTQTC--ETLKLQLPNCIEDPVSPIVLRIMPSLVGTPLSAFGNLRPVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        881 PALKREÇQVTFTINPDFNLQ-NLQNQASLSFQALSESQBENKADNLVNLKIPLLYDARI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          833 RESAYNTGIVVDFSENLFF.-----ASPGLPVDGTEVTCQVAASQKSVACDVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTBFQLELPVKYAVYMV
          LQYFGRSLDGYGDINGDSITDVSIGAFGQVVQLWSQSIADVAIEASFTFEKI--TLVNKN
                                                       DQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFNETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368;
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ilarity 22.7%; Pred. No. 7.8e-38;
Conservative 187; Mismatches 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:||| : | |:||||||:|| | GILLLLAEVAILMKLGFFKRKYYEKM 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 GLLLLALITAALYKLGFFKROYKDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STG---SCEPIRLOVP----
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tes 281, Conserv
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A.Title: Separation of important new platelet glycoproteins (GPIa, GPIc*, GPIIa an A, Reference number: A56793; MUD:92061944; PMID:1953640
A.Accession: B56793
A.Accession: B56793
A.Accession: B56793
A.Accession: B6793
A.Accession: A5793; MUD:92061944; PMID:1953640
A.Accession: A5793
A.Accession: A53117; MUD:94103255; PMID:8276836
A.Accession: A53117.
                                                                                                                                                                                                                                                                                      A; Morecule type: DNA
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Residues: 1-16, VV, 18-21 < 2UT>
A; Note: authors translated the codon GTA for residue 17 as Leu
C; Genetics: GDB: 17GA2; CD49B
A; GDB: 17GA2; CD49B
A; Map position: 5q11.1-5q11.2
A; Map position: 5q11.1-5q11.2
A; Map position: 5q11.1-5q11.2
A; Map position: squence #status predicted < SIG>
F; 10-1131/Domain: signal sequence #status predicted < SIG>
F; 10-1131/Domain: scaracellular #status predicted < EXT>
F; 112-347/Domain: von Millebrand factor type A repeat homology < VWA2>
F; 113-1154/Domain: intracellular #status predicted < CTM>
F; 113-1154/Domain: intracellular #status predicted < CTM>
F; 115-1181/Domain: intracellular #status predicted < CTM>
F; 105, 112, 343, 432, 460, 475, 699, 1057, 1074, 1081/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAIAALSDINMDGFNDVIVGSPLENQNSGAVYIYNGHQGT-IRTKYSQKILGSDGAFRSH 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDISPDF-QLSASFSPATQPCPSL-IDVVVVCDESNSIYPMD--AVKNFLEKFVQGLDIG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 ITNGARKNAPKILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVIGV-----GDAFRSEK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SROBLNTVASKPPRDHVFQINNFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRNRVQSIVLGAPRYQHIGLVAMFRQNTGMWESNANV-----KGTQIGAYFGASLCSV 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQYPGOSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVPECN 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 GSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 ATCEKLINIĞISISIPNVTEMKTAMSLGLILTRANMGTGGFLTCGPLWAQQCGNQYYTTGVC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 FLFGSNIRQOPQKFPBALRGCPQBDSDIAFLIDGSGSIIPHDFRRMKBWVSTVMBOLK-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSKTLPSIMOYSEEPRIHFTPKEFONNPNPRSLIKPITOLLG-RTHTATGLRKVVRBLFN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 PTKTQVGLIQYANNPRVVFNLNTYKTKBEMIVATSQTSQYGGDLTNTFGALQYARKYAYS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAAITSNGP---LLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYAAAI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALIVIGDVNGDKLIDVAIGAPGEEDNRGAVYLFHGISGSGISPSHSORIAGS--KLSPR 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.9%; Score 1054; DB 2; Length 1181;
llarity 26.7%; Pred. No. 3.8e-65;
Conservative 216; Mismatches 494; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 327; Conserv?
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QY 1091 -LPLIVGSSVGGLALALITAALYKLGFFKRQYKDMMSB 1128 :: :: ::	RESULT 13 S06046 integrin alpha-4 chain precursor - human N;Alternate names: CD49d; very late antigen-4 alpha chain; VLA-4 alpha chain	vision 01-Dec- 018 se C Hemler	re of the alpha(4) sul fulD:89356603; PMID:2'	AjMordeshidi Subvare AjMordeshidi type: mRMA AjResidues: 1-1038 <tak> AjCross-references: GB:X16983; EMBL:X15386; NID:g33945; PIDN:CAA34852.1; PID:g333</tak>	Afforen, G.D.; Birkenmeter, 1.7, Dean, D.; 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 4094-4098, 1991 A; Title: Characterization of the alpha-4 integrin gene promoter. A; Reference number: A39355; WUID:91239513; PMID:2034655	A.Molecule type: DWA A.Molecule type: DWA A.Residues: 1-93 <ros> A.Cross-references: GB:M62841</ros>	Ajfakada, r.; Scroninger, v.L.; Henler, W. 1987 Proc. Natl. Acad. Sci. U.S.A. 1987 Ajfitle: The very late antigen family of heterodimers is part of a superfamily of A; Reference number: A94151; MUID:87204112; PMID:3033641	A;Mccesbion: Digute A;Molecule type: protein A;Residues: 40-50, E',52-53 <ta2> C;Genetics:</ta2>	49D 203:128032; OMIM:192975 20: alpha-4 chain	C.Keywords: Cell adhesion; Cycoskeleton; duplication; glycoprotein; neterodimer; F;1-39/Domain: signal sequence #status predicted <sig> F;40-1038/Product: integrin VLA-4 alpha-4 chain #status predicted <mat></mat></sig>	Query Match 10.9%; Score 642; DB 2; Length 1038; Best Local Similarity 23.8%; Pred. No. 2.3e-36; Matches 293; Conservative 175; Mismatches 409; Indels 356; Gaps 53;	Oy 1 FNLDTENAMTEQ-ENARGEGGSVV-QLQSSRVVVGAPQEIVAANQRGSLYQCDY 52	OY 53 STGSCEPIRLQVPVBAVNMSLGLSLAATTSPPQLLACGFTVHQTCSENTYVKGLCFL 109	QY 110 FGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKGKT 169	QY 170 LFSLMQYSEBFRIHFTPKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGA 229	OY 230 RENDEKILFLIDGEKEGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQEINTVAS 289	CY 290 KPPRDHVFQI-NNFRALKTIGNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGF 348	Qy 349 LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSL 403
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96 TCSENTYVKGLCPLFGSNLRQQPQKFPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRNKR 155 	WVSTVMBQLKKSKTLFSLMQYSEBFRIHFTFKBPQNNPNPRSLIKPITQLLGRTHTATGL : : : : RMAPCYKDYT	216 RKVVRELFNITNGARKNAFKILFLLDGGKRGDPLGYSDVIPELDREGVIRYVIGVGDAF 275	276 RSEXSRQELNTVASKPPRDHVPQINNFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMS 335	336 QEGPSAALTSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINWTRVDSDWNDAYLGYA 391	392 AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTOIGAYFGASLCS 447	448 VDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPLPRGGRA-RWQCDAVLYGEQGOPWGRFG 506 ::: : :: ::	507 AALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQ 566 ::	567 YFQQSLGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECN 624	625 DQVVXGXEAGEVRVCLHYQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNET 679	680 KONSTRRQTQVLGLIQTCBTLKLQLPNCIEDPVSPIVLRLNPSLVGTPLSAFGNLR 734 :: : : :	PVLAEDAQR-LIPTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNV 1	TUTVRNDGEDSYRTQVTPFFPDDLSYRKVSTLQNQRSQRSWRLACESASSTBVSGALKST [SCSINHPIFPENSEVTENITEDVDSKASLGNKLLLKANVISENNMPRINKTEFQLELE	VXXAVYMVYTSHGV STKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFL ::	VPVRINGTVIMDRPQVTFSENLSSTCHTKERLESHSDFLAELR	RAPVINGSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEIL ::	FNDSVPTLLPGQGGAFVRSQTBTXVRPPEVPNP	934 EMDETSSLKFEIKATAFPEPHPKVIELNKDENVAHVFLEGLHHORPKRHF 983
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dimers is part of a superfamily of molec
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d <SIG>
#status predicted <MAT>
                                                                                                                                                                                                     subunit of VLA-4: homology to other inter:2788572
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                                                                                                                                          989 #text_change 24-Sep-1999
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e-36;
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in gene promoter.
:2034655
KEDMMSE 1128
|| :: |
KESILQE 1022
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A;Residues: 1-1035 <res> A;Rossidues: 1-1035 <res> A;Cross-references: GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g533327 A;Cross-references: GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g533327 R;Palmer, B.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D. J. Cell Biol. 123, 1289-1297, 1993 A;Ttle: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partn A;Reference number: A49459; MUID:94064789; PMID:8245132 A;Recession: A49459 A;Residues: 30-1035 <pal> A;Residues: 30-1035 <pal> A;Cross-references: GB:L24158 C;Superfamily: integrin alpha-4 chain C;Reywords: gJycoprotein; metal binding; transmembrane protein F;1-27/Domain: signal sequence #status predicted <sig></sig></pal></pal></res></res>	Query Match 10.7%; Score 630; DB 2; Length 1035; Best Local Similarity 26.5%; Pred. No. 1.6e-35; Matches 237; Conservative 160; Mismatches 332; Indels 164; Gaps 40;	Qy 331 BHEMSQEGFSAALITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT-RVDSDWDAYLG 389 190 BHGSCQAGIAGFFEBLVVMGAPGSFYWAGTIKVLNUTD-NTYLKLNDEVIMNRRYTYLG 248	Qy 390 YAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQ1GAYFGASL 445 	Qy 446 CSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLERGQRARWQCDAVLYGEQGQPWGRF 505	Qy 506 GAALTVLGDVNGDKLTDVALGAPGBEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRL 565 ::	Qy 566 QYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLERSQPVLRVXAIMEFNPREVARNVFBC 623 :	Qy 624 NDQVVKGKEAGEVRV-CLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAV 675	Qy 676 PNBTKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLS 728	Qy 729 APGNIAPVLAEDAQRLFTALFPERNCGNDNICQDDLSITFSFMSLDCL 777 DD 592 BLPPLTPVLRWKKGQXIAQXNQTVFERNCRSED-CAADLQLQGKLLLSSNDEKTLYL 647	Qy 778 VVGGPREFNYTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLCNQRSQRSWRLACESASS 837 :	Qy 838 TEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNK 897	Qy 898 TEPQLELPUKKAVYMVYTSHGVSTKKIAFTASENTSRVMQHQY 940
	Qy 579 TMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPRBVARNVFBCNDQVVKGKEAGBV 636	Qy 637 RVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETRRQTQVLG 691	Qy 692 EAQTCHILKIQIPNCIEDPVSPIVLRINFSLVGTPLSAFGNLRPVLABDAQR-LF 745	OY 746 TALFPEKNCGNDNICQDDLSITFSFMSLDCLVVGGFREFNVTVFWRNDGEDSY 799 519 KKTINFARFCAHEN-CSADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDDAY 677	QY 800 RIQVIPFFPLDLGYRKVSTLONQRSQRSWRLACESASSTEVSGALKSTSCSINHPIPPEN 859	QY 860 SEVTENLIFDVDSKASLGNKLLLKANVISENNMPRINKTEFQLELPVKXAVYMVVTSH 917	CY 918 GVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFLVPVRLNQTVIMDRP 971 Db 788 VNPTSFVYGSNDENEPETCMVEKMNLTFHVINTGNSMAPNVSVBIMVPNSFSP 840	CY 972 QVTFSENLSSTCHTKERLPSHSDFLAELRKAPVNCSIAVCQRIQCDIPFFGIQ 1025	QY 1026 EBENATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQG 1071	Qy 1072 AFVRSQTETKVBPFEVPNP	Qy 1096 GSSVGGLELLALITAALYKLGFFKRQYKDMMSE 1128	RESULT 14 ISBOUT 14 ISBOUT 14 ISBOUT 14 ISBOUT 14 ISBOUT alpha-9 chain precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Accession: ISBOOS R;Hibi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Takah Concogene 9, 611-619, 1994 A;Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small A;Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small A;Accession: ISBOOS A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ

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NIPLPRDFSDSTKASTLVTTEELVPVTPIAW 988
                  ----SNLGQRSLPIS------LVFLVPV 960
ELNMTVPVTVDCTLKLLSASYPEIVMYSTQED 775
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Immunol. 150:480-490(1993).
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ALIGNMENTS

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SEQUENCE FROM N.A.
MEDILISH 881910151; PubMed-2833753;
MEDILISH 881910151; PubMed-2833753;
Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
"Molecular cloning of the alpha subunit of human and guinea pig
"Heukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLINE-88257215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annaout M.A., Gupta G.K., Pierce M.W., Tenen D.G.;
"Amino acid sequence of the alpha subunit of human leukocyte adhesion
"Receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
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MEDLINE-93123748; PubMed-8419480;
Pleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
Pleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
the alpha-integrin gene family demonstrate remarkable conservation of
genomic organization and suggest early diversification during
                                                                             01-001-1989 (Rel. 11, Created)
01-007-1996 (Rel. 34, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
11ntegrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor)
11TGAM OR CR3A OR CD11B.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILIDE-883150131; PubMed=2457584;

GOTDÍ A. L., Kishimoto T.K., Miller L.J., Springer T.A.;

"The human leukocyte adhesion glycoprotein Mac-1 (complement recetype 3. CD11b) alpha subunit. Cloning, primary structure, and type 3. CD11b) alpha subunit. Cloning, primary structure, and tatation to the integrins, von Willebrand factor and factor B.";

Telation Chem. 263:12403-12411(1988).
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MEDLINE-89098893; PubMed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
PRT; 1152 AA
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
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GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WWP_A.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Pfam; PP00357; integrin A; 1.
Pfam; PP00052; vwa; 1.
PRINTS; PR01185; INTEGRINA.
SWART; SM00191; Int_alpha; 4.
SWART; SM001327; VWA; 1.
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PIR; A31108; RWHU1B.
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DR PDB; 1BHO; 18-NOV-98.
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DR PDB; 1LDN; 25-NOV-98.
DR PDB; 1LDN; 01-AUG-96.
R PDB; 1LDN; 01-AUG-96.
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PDB; 1MIU; 07-AUG-02.
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       MEDLINE=98226734; PubMed=9560195;

Oxvig C., Springer T.A.;

Oxvig C., Springer T.A.;

Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. US.A. 95:4470-4875(1998).

LI FUNCTION: INTEGRIN ALPHA-NIBERA-2 IS IMPLICATED IN VARIOUS
ADHESIVE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES
AS WELL AS IN MEDIATING THE UPPAIR OF COMPLIANT-COATED PARTICLES.

IT IS IDENTICAL WITH CR.3. THE RECEPTOR FOR THE IC3B FRAGHENT OF
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECORDEDS THE R-G-D
PEPTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR
THEINTOCHN X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES
C-I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-M
ASSOCIATES WITH BETA-2.

--- SUBCELLULAR LOCATION: Type I membrane procein.

--- SUBCELLULAR LOCATION: Type I membrane procein.

--- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
GRANULOCYTES.

--- DOMAIN: THE INTERRIN - INDOMAIN. INTEGRINS
C--- DOMAIN: THE INTERRIN - INDOMAIN. INTEGRINS
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95171458; PubMed=7867070;
Lee J.O., Rieu P., Arnacut M.A., Liddington R.;
Crystal structure of the A domain from the alpha subunit of integrin
CR3 (CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE=5635671; PubMed=8747460;
Lee J.O., Bankston L.A., Armaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE=98362595; PubMed=9867375;
Baldwin B.T.; Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model assessment.",
                                                                                                                                                                                                                                                            MEDEINE=87076671; PubMed=3539202; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; Pierce M.W., human leukocyte glycoprotein Mol: onservation across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
 SEQUENCE OF 1-9 FROM N.A.

MEDLINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                       MEDLINE-92144986; PubMed=1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 1 WWPA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
DATABASS: NAME=PROW; NOTE-CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
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SWISS-PROT entry is copyright. It is produced through a collaboration
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MEDLINE=85188276; PubMed=3887182;
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                                                                                                                                                                                                                                                                                           EMBO J. 7:1371-1378(1988).
                                                                                                    STANDARD;
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P0555;
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Springer T.A., Teplow D.B., Dreyer W.J.;

Springer T.A., Teplow D.B., Dreyer W.J.;

RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion adequence homology of the LFA-1 and Mac-1 leukocyte interferon.";

L addesing and unexpected relation to leukocyte interferon.";

L hature 314:540-542(1985).

LI STATEGRIN ALPHA-M/BETA-Z IS IMPLICATED IN VARIOUS

ADHESIVE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES

ADHESIVE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES

IT IS IDENTICAL WITH CR.3, THE RECEPTOR FOR THE ICES FRACHENT OF

THE THIRD COMPLEMENT COMPONENT. IT PROGRABLY RECCANIZES THE R-G-D

PEPTIDE IN (3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR

THE TRIBLOGEN, FACTOR X AND ICAMI. IT RECCONIZES PI AND PS PEPTIDES

OF FIBRINGEN GAMMA CHAIN. ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN

MAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-MEDIATED

GLOMERULONEPHRITIS. MICH EXPRESSING A NULL MUTATION OF THE ALPHA-M

C SUBRUIT GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMILATION, IN

RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT

APPARENTLY.

ORBESTITY.
1036 PFGIQBEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1095
                                                                                                                                        KVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKROYKDMMSEGGPPGAEPQ 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
11thegrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                               KVEPFEVDNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKOM/SEGGPPGAEPQ
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MEDLINES6819312; PubMed=294294;

Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,

Larson R.S., Roberts T.M., Springer T.A.;

An partial genomic DNA clone for the alpha subunit of the mouse

complement receptor type 3 and cellular adhesion molecule Mac-1.";

Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBL_TaxID=10090;
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES
GRANULOCYTES.
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420 436 480 496 540 555 600 615 999 675

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us-09-902-481b-4.rsp

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PLOVPPEAVNMSLGLSLAVSTVPQQLLACGPTVHQNCKENTYVNGLCYLFGSNLLRPPQQ
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A Miller L.G., Wiebbe M., Springer T.A.;

"Purification and alpha subunit N-terminal sequences of human Mac-1

"Purification and alpha subunit N-terminal sequences of human Mac-1

"I mundol. 138-2381-2383(1987).

I J Immunol. 138-2381-2383(1987).

I J IMMUNOL. INTEGRIN ALPHA-X/BETA-2 IS A RECEPTOR FOR FIBRINOGEN. IT RECORTIZES THE SEQUENCE G-PR IN FIBRINOGEN. IT MEDIATES CELL-CELL INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

INDORTANT IN MONOCYTE AND CHEMOTAXIS.

-1- SUBGENIT: HETERODIMER OF AN ALPHA AND A BETA SUBGNIT. ALPHA-X ASSOCIATES WITH BETA-2.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: PREDOMINATLY EXPRESSED IN MONOCYTES AND GRANULOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A WWPA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDESECO PROTEAGE CLEAVAGE.
SWILTH I-DOMAINS DO NOT UNDESECO PROTEAGE CLEAVAGE.
SMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 WWPA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
BATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88166645; PubMed=3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
"CDNA cloning and complete primary structure of the alpha subunit of an leukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987).
                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein pl50,95
alpha chain) (Leukocyte adhesion receptor pl50,95) (CDl1c) (Leu MS).
ITGAX OR CDl1C.
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corbi A.L., Garcia-Aguilar J., Springer T.A., J. Biol. Chem. 265:12750-12751(1990).
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EMBL; Y00093; CAA68283.1; -.
EMBL; M29165; -; NOT ANNOTATED CDS.
EMBL; M29487; AAA11620.1; ALT SEQ.
EMBL; M29482; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29484; AAA31620.1; JOINED.
EMBL; M29485, AAA51620.1; JOINED.
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J. Biol. Chem. 265:2782-2788(1990)
                                                 STANDARD;
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P20702;
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PROSITE; PS50234; VWPA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Magnesium; Calcium; Repeat; 3D-structure.

SIGMAL
20 1163 INTEGRIN ALPHA-X.
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                                           MIM, 151510; ...
GO; GO:0008105; C:integrin complex; TAS.
GO; GO:0004805; F:cell adhesion receptor activity; TAS.
GO; GO:0004805; F:cell adhesion; TAS.
GO; GO:0004155; P:cell adhesion; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR001301; Integrin_A; I.
Print; PR00185; Integrin_A; I.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00181; Int alpha; S.
SMART; SM00127; VWA; I.
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EXTRACELLULAR (POTENTIAL)
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PDB; 1N3Y; 18-FEB-03.
Genew; HGNC:6152; ITGAX.
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-1- SUBUNIT: HETERRODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D ASSOCIATES WITH BETA-2.

-1- SUBUNIT: HETERRODIMER LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: EXPERSEED MODERATELY ON MYELOWONCYTIC CELL LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON TISSUE-SPECIALIZED CELLS, INCLUDING MARNOPHAGES POAM CELLS WITHIN ATHEROSCIERCTIC PLAQUES, AND ON SPIENIC RED PULP MACROPHAGES.

-1- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

-1- SIMILARITY: Contains 1 VWFA domain.

-1- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDILINE=9625725; PubMed=8666289; Mong D.A., Davis B.M., Lebeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
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                                                                                                                                                                                   TISSUB-Spleen;
MEDLINE=56111956; PubMed=8777714;
MEDLINE=56111956; PubMed=8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.B., Gallatin W.M.;
**A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoffman P.A.,
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-!- FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND VOAM1. MAY PLAY A ROLE IN THE ATHENOSCILEROTIC PROCESS SUCH AS CLEARING LIPOPROTRIES FROM PLAQUES AND IN FHAGOCYTOSIS OF BLOOD-BORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH VCAMI.
MEDLINE=99370002; PubMed=10438935;
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for binding interface between I domain and VCAM-1.";
                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDLINE-99059842; Pubbed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gall; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gall; Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and fur as an alternative ligand for vascular cell adhesion molecule I (VCAM-1)";
               â
                 (Leukointegrin alpha
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta 2-integrin alpha subunit.";
Gene 171:291-294 (1996).
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                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
             Integrin alpha-D precursor
                                                                                                                                                                                                                                                                                                                                                       OF 1-235 FROM N.A.
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                                                            sapiens (Human)
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EXTRACELLULAR (POTENTIAL).

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FG-GAP 4.

FG-GAP 6.

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V -> A (IN REF. 2).
MW; F296AlA35455D77D CRC64;
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CDITA I-domain.";
J. Mol. Biol. 292:1-9(1999).
J. Mol. Biol. 292:1-9(1999).
J. FUNCTION: INTEGRIN ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAMI, ICAM2,
I-FUNCTION: INTEGRIN ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAMI, ICAM2,
ICAM3 AND ICAM4. IT IS INVOLVED IN A VARIETY OF IMMUNE PHENOMENA
INCLUDING LEUKOCYTE-ENDOTHELIAL CELL INTERACTION, CYTOTOXIC T-CELL
MEDIATED KILLING, AND ANTIBODY DEPENDENT KILLING BY GRANUL/CCYTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.
MEDLINE-99425288; PubMed=10493852;
Kallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G.,
Cottens S., Welzer-Schmidt G., Hommel U.;
"Structural basis for LFA-1 inhibition upon lovastatin binding to the
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDLINE=89139587; Pubmed=2537322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99425270; PubMed-10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Fubraman J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Bichler B.B., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from
Genomics 60:295-308(1999).
                                                                                                             TTAL HUMAN STANDARD; PRT; 1170 AA.
P20701; 043746;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Integrin Alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (Leukocyte function associated molecule 1, alpha chain)
(CD11a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=96398682; PubMed=8805579;

Qu A., Leahy D.J.;

The role of the divalent cation in the structure of the I domain from the CD11a/CD18 integrin.";

Structure 4:931-942(1996).
                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-L
ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  superfamily.";
J. Cell Biol. 108:703-712(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Note=No experimental confirmation available;
ISSUE SPECIFICITY: LEUKOCYTES.
DOMAIN: THE INTEGRIN I LOOMAIN INSERT) IS A WHPA DOMAIN. INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGO; GO: 0006926; C: integrin complex; TAS.

RGO; GO: 0006926; P: cell motility; TAS.

R GO: GO: 0006928; P: cell motility; TAS.

R InterPro; IPR002035; WWF.A.

R Pfam; PR01839; FG-GAP; 3.

R Pfam; PR003057; integrin.A: 1.

R Pfam; PR003057; integrin.A: 1.

R R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR01091; Int. alpha; 4.

R SMART; SM00191; Int. alpha; 4.

R RART; SM00191; Int. alpha; 4.

R R SMART; SM00191; INTEGRIN.

R PROSITE; PS0224; WWA; 1.

R PROSITE; PS0224; WWA; 1.

R PROSITE; PS10186;                                                                       -!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 1 WAFA domain.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
-|- DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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PG-GAP 5.
PG-GAP 6.
FG-GAP 7.
PG-GAP 7.
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FG-GAP 2.
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PDB; 1MQ9; 14-JAN-03.
PDB; 1MQ9; 14-JAN-03.
Genew; HGMC:6148; ITGAL.
MIM; 153370;
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07-DEC-96.
07-DEC-96.
07-DEC-96.
07-AUG-00.
03-FEB-00.
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PDB, 1DGQ;
PDB, 1MJN;
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345 KIHQVKHMYQVRIQPSIHDHNIPTLEAVVGVPQPPSEGPITHQWSVQMEPPV--PCHYED 1002
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                                SYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQH
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TAL MOUSE

AC P24063.

AC P24063.

DT O1-MAR-1992 (Rel. 21, Created)

DT O1-MAR-1992 (Rel. 21, Last sequence update)

DT 28-FBB-2003 (Rel. 41, Last annotation update)

DR Isegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1

DB alpha chain) (Leukocyte function associated molecule 1, alpha chain)
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Trada. OR. LPA-1.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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O -> OGVHGLVENONISKQLICREAGDNEHWGAQGGLPC
PWGVSEAFRDNIRAGPCR (in isoform 2).
/PTIG-VSP 002738.
R -> W (IN REF. 1).
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                                                                                                     LEUCOCYTES RECRUITMENT.
SUBUNT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-L
ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
ITSSUE SPECIFICITY: LEUKOCYTES.
DOMAIN: THE INTEGRIN LOCATION: INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains I WFPA domain.
SIMILARITY: Contains 7 FG-GAP repeate.
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R RASP, P20011; ILFA.

R MGD, MG1:96606, Itgal.

R InterPro; IPR000013; INtegrin_alpha.

R InterPro; IPR000135; VWF A.

R Pfam; PF001839; RG-GAP, 3.

R Pfam; PF00185; INTEGRINA.

R PRINTS; PR00145; VWFADOWAIN.

R PRINTS; PR00145; VWFADOWAIN.

R SWART; SW00019; INTEGRINA.

R PROSITE; PS50242; INTEGRINA.

R PROSITE; PS50243; NWFA. 1.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
FG-GAP 2.
                                          Kaufmann Y., Tseng E., Springer T.A.; "Cloning of the murine lymphocyte function-associated alpha-subunit and its expression in COS cells."; J. Immunol. 147:369-374 (1991).
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
                                                                         J. Immunol. 147:369-374(1991).
SEQUENCE OF 24-42.
MEDLINE-85188276; PubMed=3887182;
                              SEQUENCE FROM N.A.
MEDLINE=91268576; PubMed=2051027;
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al Similarity 34.1%; Pred. No. 4.5e-94;
398; Conservative 217; Mismatches 463; Indels
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                                                                                                                                                                                                                                                                                                                      LLKANVTSEN-NMPRTNKTBPQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQ 939
                                                                                                                                                                                                                                                                                                                                          888 ELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTQQVQHV 947
                                                                                                                                                                                                                                                                                                                                                                                           YOVSNIGORSIPISIVFIVPVRINQTVIWDRPQ----VTFSENISS----TCHTKE-RIP 990
MEDLIRE=95107992; PubMed=7882170;
Smith T.J. Ducharme L.A., Shaw S.K., Parker C.M., Brenner M.B.,
Kilehaw P.J., Weis J.H.;
Kilehaw P.J., Weis J.H.;
Immunity 1:393-403(1994)
Immunity 1:393-403(1994)
Immunity 2:393-403(1994)
Immunity B.S. ARCEPTOR FOR E-CADHERIN. IT
FUNCTION: INTEGRIN ALPHA-E/BETA-7 IS A RECEPTOR FOR E-CADHERIN. IT
MEDIATES ADHESION OF INTRA-EPITHEIAL T-LYMPHOCYTES TO BPITHELIAL
CELL MONOLAYERS. MICE EXPRESSING A NULL MUTATION OF THE ALPHA-E
SUBBUIT GENE EXHIBET A MARKED REDUCTION IN THE NUMBERS OF
INTRAEPITHELIAL LYMPHOLYTES IN THE GUT AND IN THE DEVELOPMENT OF
GUT-ASSOCIATED LYMPHOLD AGGREGATES, SUPPORTING A SPECIPIC ROLE FOR
                                                  EGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV
                                                                       OGRILANLSYTLQLDGHRWRSRGLFPDGSHBLSGWTSITP-DKSCLDFHFHFPLCIQDLI
                                                                                                                                                                                                         SSPARS-----GPLRIMSSASILAVEWTLSNSGEDAYWVRLDIDFPRGLSFRKVEMLQ-
                                                                                                                   SPIVLRINFSLV---GTPLSAFGN-LRPVLAEDAQRIFTALFPFEKNCGNDNICQDDLSI
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SUBCELLULAR LOCATION: Type I membrane protein.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIS INTEGRIN IN MEDIATING RETENTION OF LYMPHOCYTES IN THE INTESTINAL WALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Integrin alpha-E precursor (Integrin alpha M290).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anmounce/or send an email to license@isb-sib.ch).
-!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                           MCD. MGI.1298377; Itgae.

MGD, MGI.1298377; Itgae.

R InterPro; IPR0000413; Integrin_alpha.

R InterPro; IPR000035; VWF A.

R Pfam; PR01839; PG-GAP; 3.

R Pfam; PR01857; integrin_A; 1.

R Pfam; PR01857; integrin_A; 1.

R PRINTS; PR0185; INTEGRINA.

R SWART; SM0019; INTEGRINA.

R R SWART; SM0019; INTEGRINA.

R PROSITE; PS50242; INTEGRIN_ALPHA; 1.

R PROSITE; PS50242; INVERIN_ALPHA; 1.

R PROSITE; PG50242; INVERIN_ALPHA; 1.

R PROSITE; PG50242; INVERIN_ALPHA; 1.

R PROSITE; RF0041; Cell adhesion; Receptor; Glycoprotein; Transmembrane;

M Signal; Repeat; Magnesiun;
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(POTENTIAL).
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INTEGRIN ALPHA-E.
INTEGRIN ALPHA-E LIGHT CHAIN.
INTEGRIN ALPHA-E HEAVY CHAIN.
EXTRACELLULAR (POTENTIAL).
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GLU-RICH (ACIDIC).
GREEN MOTH.
BY SIMILARITY.
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986 KERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPPFGIQEEFNATIKGNLSFDWYIKTS 1045
                                                                                                                                                 1026 SQRPACGSDPVQHVKEWERSVVCAI-----TSNKENVTVAAEISVG
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-!- FUNCTION: INTEGRIN ALPRA-E/BETA-7 IS A RECEPTOR FOR E-CADHERIN. IT
-!- FUNCTION: INTEGRIN ALPRA-E/BETA-7 IS A RECEPTOR FOR E-CADHERINAL T-LYMPHOCYTES TO EPITHELIAL.
CELL MONOLAYERS.
-!- SUBUNIT: HETERODINER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
SUBUNIT: HETERODINES OF AN HEAVY AND A LIGHT CHAINS LINKED BY A
DISULPIDE BOND. ALPHA-E ASSOCIATES WITH BETA-7.
                    1046 HNHLLIVSTA-----EILFNDSVPTLLPGQGAFVRSQTETKVEPF----EVPNPLPLIV
DSKASLGNKLLLKANVTSENNMPRTNKTEPQLELPVKYAVYMVVTSHGVSTKYLNFTASE
                                                              NTSRVMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSBNLSST----CHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGENESIS OF ASP-109 AND PHE-316.
MEDLINE=20400502; PubMed=10837471;
Higgins J.M.H., Cernadas M., Tan K., Irie A., Wang J.-H., Takada Y.,
Brenner M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Touchman J.W., Anikster Y., Dietrich N.L., Maduro V.V., McDowell G. Shotelersuk V., Bouffard G.G., Beckstrom-Sternberg S.M., Gahl W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Leukemia, and Lymphocytes;
MRDIINE-24164962; PubMed-8119947;
MBAW S.K., Cepek K.L., Murphy B.A., Russell G.J., Brenner M.B.,
Parker C.M.;
Parker C.M.;
Wholecular cloning of the human mucosal lymphocyte integrin alpha
subunit. Unusual structure and restricted RNA distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genomic region encompassing the nephropathic cystinosis gene (CTNS): complete sequencing of a 200-kb segment and discovery of a novel gene within the common cystinosis-causing deletion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen) (HML-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 19-38 AND 179-188.
                                                                                                                                                                                                                                                                                                                                                        ITAE HUMAN STANDARD; PRT; 1179 AA. P38570; QSNZU9; 01-0CT-1994 (Rel. 30, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Integrin alpha-E precursor (Mucosal lymphocyte-lantigen) (CD103 antigen) (Integrin alpha-IEL). ITGAE.
                                                                                                                                                                                                                                                               GSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
                                                                                                                                                                                                                                                                             subunit. Unusual structure and rest:
J. Biol. Chem. 269:6016-6025(1994).
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MEDLINE=20138496; PubMed=10673275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 SKLQQRIVHMEGT---VGDALQYQLAQTGFSAQILDKGQVLLGTVGAFNWSGGALLKSTQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 KEKSTEINMT-RVDS-DWNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGM 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQRARWQCDAVLYGBQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP-----GBBDNRGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QDASPSLAHTLSGHPGLTNSRPGPAMAAVGDINQDKFTDVALGAPLEGFGAGDGASYGS 606
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                                                                                                                                                  1 FNLDTENA--MTPQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGS-----LYQCDY
                                                                                                                                                                                                                                                                                FGSNIRQOPQKFPEALRG
                                                                                                                                                                                                                                                                                                                                                 132 DSDIAFLIDGSGSIIPHDFRRMKEWVSTVMRQL--KKSKTLFSLMQYSBBFRIHFTFKEF
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                                                                                                                 Gape
                                                                                19.5%; Score 1148.5; DB 1; Length 1167; 28.8%; Pred. No. 1.1e-68; ive 214; Mismatches 459; Indels 205;
 (GLCNAC, .) (POTENTIAL) (GLCNAC, .) (POTENTIAL) (GLCNAC, .) (POTENTIAL)
                                                  MW; B8331C115DCCCFFD CRC64;
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Best Local Similarity 28.89
Matches 355; Conservative
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON A SUBCLASS OF T-LYMPHOCYTES KNOWN
AS INTRA-EPITHELIAL LYMPHOCYTES WHICH ARE LOCATED BETWEEN MUCOSAL
EPITHELLAL CELLS.
DOWAIN: THE INTEGRIN I-DOWAIN (INSERT) IS A WWFA DOWAIN. INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 WWFA domain.
SIMILARITY: COntains 7 FG-GAP repeats.
DATABASE: NAME-PROW; NOTE=CD guide CD103 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd103.htm".
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL). (POTENTIAL). (POTENTIAL).
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FG-GAP 4.

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FG-GAP 7.

POTENTIAL.

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RY SIMILARITY

BY SIMILARITY
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EMBL; AF168787; AAF43107.1; --
EMBL; AF168787; AAF43107.1; --
EMSP; P11215; A53213.
ESSP; P1215; A68X.
Genew; HGNC:6147; ITGAE.
MIM; 604682; ---
GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0008495; F:cell adhesion receptor ac
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
PFam; PP00397; VWP.A.
PFam; PP00397; VWP.A.
PRINTS; PR00185; Integrin_A; 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00185; INTEGRINA.
PRNTT; SM00191; Int. alpha; 3.
SWART; SM00191; Int. alpha; 3.
SWART; SM00191; INT. alpha; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
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                                                                                                                                                                                                                                                                                                                                                                    65 GPLARCSLVQDBILCHPVEHVPIPKGRHRGVTVVRSHHGVLICI-----QVLVRRP--HS
                                                                                                                                                                                                                                                                                                                                                                                                                    285 NIVASKPPRDHVFQINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 CSLSYVAGAPQYKHG--AVFELÇKEGREASFLPVLEGEÇMGSYPGSELCPVDIDMDGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGGQPWGRFGAALTVLGDVN
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                                                                                                                                                                                                                                                                                                                                                                                                    96 TCSENTYVKGLCFLFGSNLRQQPQ------
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                                                                                                                                                                                                                                                                              19.4%; Score 1140; DB 1; Length 1179;
ilarity 28.9%; Pred. No. 4.1e-68;
Conservative 214; Mismatches 451; Indels 172; Gaps
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                               Similarity
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1. SHOUTHLY.

1. SHOLL Chem.

268:2989-2996(1993).

1. FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-B-R IN COLLAGEN.

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1 ASSOCIATES WITH BETA-1.

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1

2. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1

2. SUBULARITY: Contains 1 VWFA domain.

3. SIMILARITY: Contains 1 VWFA domain.

4. SIMILARITY: Contains 7 PG-GAP repeats.

5. SIMILARITY: Contains 7 PG-GAP repeats.

6. SIMILARITY: Contains 7 PG-GAP repeats.

7. SIMILARITY: Contains 7 PG-GAP repeats.

8. SIMILARITY: Contains 7 PG-GAP repeats.

8. FWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd49a.htm".

8. PBB: 10CS: 17-MAY-00.

8. PBB: 10CS: 17-MAY-00.

8. PBB: 10CS: 17-MAY-00.

8. PBB: 10CS: 17-MAY-00. NLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFWATLKGNLS 1037 PDWYIKTSHNHLLIVST-----ARILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPL 1091 924 VWQLEENAFPNRTADITVTVTNSNERRSLANETHTLQFRHGFVAVLSKPSIMYVNTGQGL 983 757 SGSQLCEDL-LLMPTEGELCEEDCFSNASVKVSYQL-QTPEGQTDHPQPILDRYTEPFAI 814 867 TFDVDSKASLGNKLLLKANVTSENN----MPRTNKTEFQ---LELPVKXAVYMVVTSHGV 919 S--TKYINFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSE 977 YPRNLQ-----LKRMQKPPSPNIQCDDPQPV---ASVLIMNCRIGHPVL-KRSSAHVSV ALPPERNOGNDNI CODDLSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFF FPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNI SEQUENCE FROM N.A. MEDAMED=8428973; MEDINE=99155124; PubMed=8428973; MINIONE=99152124; PubMed=8428973; MINIONESEWITZ R., Epstein M.R., MINIONESEWITZ R., Epstein M.R., MINIONESEWITZ R., Epstein alpha "Expression of native and truncated forms of the human integrin alpha Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2013 (Rel. 42, Last annotation update)
111cegrin alpha-1 (anninin and collagen receptor) (VLA-1) (CD49a) GO: GO:0008305; C:integrin complex; TAS.
GO: GO:0004895; F:cell adhesion receptor activity; NAS.
GO: GO:0005518; F:cellagen binding; TAS.
GO: GO:0005160; P:cell-matrix adhesion; NAS.
InterPro; IPR000413; Integrin_alpha. PLIVGSSVGGLILLALITAALYKLGPFKROYKDMASE 1128 STANDARD; HUMAN 1 subunit. J. Biol. C 874 1038 1092 1126 747 807 920 978 ITGA1. ITA1 HUMAN g 셤 g ઠે 용 임 g ò 8 8 ö È 8

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107 CPLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRNKEWVSTVMBQLKK 166
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InterDro; IPR002035; VWF.A.
Pfam; PF01839; RG-GAP; 3.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00357; VW4; 1.
SWART; SW00191; Int.alpha; 5.
SWART; SW00242; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
Repeat; Calcium; Receptor; Glycoprotein; Transmembrane; Repeat; Calcium; BIT13 EXTRACELLULAR (POTENTIAL).
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Andreu N., Betivill X., Becarceller M., Sumoy b.;
Andreu N., Betivill X., Becarceller M., Sumoy b.;
Submitted (JUN-2000) to the EMEJ/GenBank/DDBJ databases.
-1- FUNCTION: INTEGRIN ALPHA-11/BETA-1 IS A RECEPTOR FOR COLLAGEN.
-1- SUBMUTT: HETRODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-11
ASSOCIATES WITH BETA-1.
-1- SUBGLILLAR LOCATION: Type I membrane protein.
-1- SIBGELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: ACCORDING REP. 2 HIGHEST LEVELS IN UTERUS AND HEART, INTERMEDIATE LEVELS IN SKELETAL WISCIE AND INTERMEDIATE TO LON LEVELS IN SKELETAL WISCIE AND LEVELS IN SKELETAL MUSCIE AND LEVELS IN SKELETING. STOWAGE, TESTIS, SALIVARY GLANDS, THYROID GLANDS AND PROSTATE. VERY LOW LEVELS IN PRESTINGS AND PROSTATE. VERY LOW LEVELS IN PRESTINGS AND PROSTATE. VERY LOW LEVELS IN PRESTINGS AND PROSTATE. LIVER.
--- PETAL MUSCIE CELLS (IN VITRO).
--- DOWAIN: THE INTEGRIN 1-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH 1-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
--- SIMILARITY: Contains 1 VWFA domain.
--- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       TISSUE=Fetal heart, and Osteoblast;
MEDELMES99417678; Fubmed=10486209;
Lehnert K., Ni J., Leung E., Gough S.M., Weaver A., Yao W.P., Liu D.,
Wang S.-X., Morris C.M., Krissansen G.W.;
Manj S.-X., Morris C.M., Krissansen G.W.;
"Cloning, sequence analysis, and chromosomal localization of the novel
human integrin alphal1 subunit (ITGAll).";
Genomics 60:179-187(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Fetal muscle, and Uterus;
MEDLINE-99395147; PubMed=10464311;
Velling T., Kusche-Gullberg M., Sejersen T., Gullberg D.;
Velling and Chromosomal Localization of Human alpha(11)
Integrin. A collagen-binding, i domain-containing, beta(1)-associated integrin alpha-chain present in muscle tissues.";
J. Biol. Chem. 274:25735-25742(1999).
                                                                                                                                                               Craniata, Vertebrata, Buteleostomi;
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0008305; C:integrin complex; TAS.
GO:0004895; F:cell adhesion receptor activity; TAS.
               OUNCE; 09UKO1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last annotation update)
Integrin alpha-11 precursor.
1189
PRT;
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EMBL; AP137378; AAD51919.2; -.
EMBL; AL359064; CAB94392.1; -.
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Mammalia; Eutheria; Primates;
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Genew; HGNC:6136; ITGAll.
  STANDARD;
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28-FEB-2003 (Rel. 41, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa)
(Collagen receptor) (VLA-2 alpha chain) (CD49b) (Fragment).
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CSVDVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWG 503
                                                                                                                                                         ECNDOVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFN 677
                                                                                                                                                                                                                                                                                                        ETKNSTRRQTQVLGLTQTCE--TLKLQLPNCIEDPVSPIVLRLNFSL--VGTPLSAFGNL 733
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                                                                                                                                 AFGAALTVIGDVNGDKLIDVAIGAPGBEDNRGAVYLFHGISGSGISPSHSQRIAGS--KL 561
                                                                                 SPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMBFNPREVARNVF
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia)
(Collagen receptor) (VLA-2 alpha chain) (CD49b).
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SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Lung;
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1141 ILWKLGFFKRKYEKM 1155
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSOCIATES WITH BETA-1.

- SUBSCELLULAR LOCATION: Type I membrane protein.

- OWBSELLULAR LOCATION: Type I membrane protein.

- DOMAIN: THE INTERRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTECRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

- INILARITY: Belonge to the integrin alpha chain family.

- SIMILARITY: Contains 1 VWFA domain.

- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                       MEDLINE=94355691; PubMed=7521231;
Wu J.E., Santoro S.A.;
"Complex patterns of expression suggest extensive roles for the alpha "Complex patterns of expression suggest extensive roles for the alpha 2 beta 1 integrin in murine development.";
Dev. Dyn. 199:292-14(1994).
-!- FUNCTION: INTEGRIN ALPHA-2/BETA-1 IS A COLLAGEN RECEPTOR, BEING RESPONSIBLE FOR ADHESION OF PLATELETS AND OTHER CELLS TO COLLAGENS, MODULATION OF PLATELETS AND OTHER CELLS TO FORCE GENERATION AND ORGANIZATION OF NEMLY SYNTHESIZED EXTRACELLULAR MATRIX. IT IS ALSO A RECEPTOR FOR LAMININS, COLLAGEN C-PROPERTIDES AND B-CADHERIN. MICE HOMOSYGOUS FOR A NULL MUTATION IN THE ALPHA-2 DIE VERY EARLY IN EMBRYOGENESIS.
-!- SCHULT; HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-2
                Edelman J.M., Chan B.M., Uniyal S., Onodera H., Wang D.Z., Damjanovich L., Latzer D.B., Finberg R.W., Bergelson J.M.; The mouse VLA-2 homologue supports collagen and laminin adhesion but not virus binding: 2:131-143(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin, Cell adhemin, Receptor, Glycoprotein; Transmembrane, Platelet, Signal, Repeat, Calcium, Magnesium.
SIGNAL 1 26 BY SIMILARITY.
CHAIN 27 1179 ENTEGRIN ALPHA-2.
DOWAIN 27 1129 EXTRACELLULAR (POTENTIAL).
TRANSMEM 1130 1151 POTENTIAL.
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GFFKR MOTIF.
BY SIMILARITY.
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MSJ, MGI:96600, Itg2.

MSJ, MGI:96600, Itg2.

InterPro; IPR000413; INTEGRIn_alpha.

InterPro; IPR002035; VWF A.

Pfam; PF00183; FG-GAP; 3.

Pfam; PF00183; integrin_A; 1.

Pfam; PF00192; VWA; 1.

PKART; SM00191; Int_alpha; 4.

PKOSITE; PS00242; INTEGRIN_ALPHA; 1.

PROSITE; PS50234; VWFA; 1.
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FG-GAP 2.
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FG-GAP 3
FG-GAP 4
FG-GAP 5
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MEDLINE=94363406; PubMed=8081889;
                                                                                                                                                                          [2]
SEQUENCE OF 450-1178 FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z29987; CAA82877.1; -. EMBL; X75427; CAA53178.1; -. PIR; S44142.
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1081 FAASTFQTVQLTAAAEIDTHNPQLFVIBENAVTIPLMIMKPTEKAEVPT--GVIIGSIIA 1138
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                                                                                                                                                      ----ASFSMPVDGTEVTCEVGSSQKSV 871
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DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
WITH I-DOMAINS DO NOT UNDERGO PROTEACE CLEAVAGE.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains I VWFA domain.
SIMILARITY: Contains 7 FG-GAP repeats.
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MEDLINE=99313197; PubMed=10386626;
Nolte M., Pepinnsky R.B., Venyaminov S.Y., Koteliansky V.,
Gotwals P.J., Karpusas M.; Palphalbetal integrin I-domain: insights into integrin I-domain function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 452:379-385(1999).
-!- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND
-:- COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-
                                                                                                                                                                                                                                                                              956 FLV-------PVRINQTVIMDRPQVTF-SENLS
RAYSETUKVPSIPFYKECGSDGICISDLILDVQQLPAIQTQSF----IVSNQNKRLTFS
                                                                                                                               SCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTE--FQLELP
                                                      VIVRNDGEDSYRIQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSI-EVSGALKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ignatius M.J., Large T.H., Houde M., Tawil J.W., Barton A., Esch F., Carbonetto S., Reichardt L.F.; Molecular cloning of the rat integrin alpha 1-subunit: a receptor for laminin and collagen.";
J. Cell Biol. 111:709-720(1990).
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01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Integrin alpha 1 precursor (Laminin and collagen receptor) (VLA-1)
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                                                                                                                                                                                                       VKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR-----
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MEDLINE=90338125; PubMed=2380249;
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Rattus norvegicus (Rat)
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Republ; 10x4; 03-M3720.

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Reptan; PF01035; VWF A.

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Reptan; Reptan; Calcium; Receptor; Glycoprotein; Transmembrane; Signal; Reptan; Calcium; Magnesium; 3D-structure.
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                                                                                                                                                                                                                                                316 GNLSTEKFVERIKSIASEPTEKHFFNVSDELALVTIVKALGERIFALEATADQSAASFEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDVDSNGSTDLVLIGAPHY------YBQTR-GGQVSVCPLPRGQRARWQCD
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                                                                             FIVUDUKUSMSFSGPVEDMFGYTVQQYENEEGKRVLIGSPLVGQPKARTGDVYKCPVGRER
                                                                                                                                                                     CFLFGSNIRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVM---EQ
                                                                                                                                                                                                                             164 LKK----SKTLPSLMQYSBEPRIHFTFKBFQNNPNPRSLIKPITQLLG-RTHTATGLRK
                                                                                                                                                                                                                                                                                                                                           ----SEKSROBLNTVASKPPRDHVFQINNPBALKTIONOLREKIFAIEGTQTGSSSSFEH
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                                                        1 FNLDTENNATPOENARG-FGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQCDYSTGS
                                                                                                              57 CEP-IRLQVPVEA-----VNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGL
                                                                                                                                                                                                                                                                                     218 VVRELFNITNGARKNAPKILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFR-
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   tch 17.9%; Score 1055; DB 1; Length 1180; al Similarity 27.4%; Pred. No. 2e-62; 346; Conservative 196; Mismatches 475; Indels 246;
Length 1180;
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1068 PGQGAFVRSQTETKVEPPEVPNPLPL--IVGSSVGGLLLLALITAALYKLGFFKRQYKDM 1125
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                                                                                                    972 -----QVIFS------ENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQ
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11ntegrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa)
(Collagen receptor) (VLA-2 alpha chain) (CD49b).
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--- FUNCTION: INTEGRIN ALPHA-Z/BETA-1 IS A RECEPTOR FOR LAMININ,
--- COLLAGEN O. --- PROPEPTIDES, PIBRONECTIN AND B-CADHERIN. IT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MBDLINE=98019223; PubMed=9353312;
Emsley J., King S.L., Bergelson J.M., Liddington R.C.;
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MEDLINE-94043762; PubMed-7901236;
Santoso S., Kalb R., Walka M., Kiefel V., Mueller-Eckhardt C.,
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TISSUE-Endothelial cells;
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J. Clin. Invest. 92:2427-2432(1993).
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- EXTRACLIDIAR WATKAIA.
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- SUBCELLULAR WATKAIA.
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- DOMAIN: THE INTEGRIN: Type I membrane protein.
- DOMAIN: THE INTEGRIN: Type I WEBERT IS A WHYA DOWAIN. INTEGRINS WITH I-DOMAIN: DOWAIN SA IS ASSOCIATED WITH DIATHORPHISM: POSATION 534 is associated with platelet-specific alloantigen HPA-5 (BR). HPA-5A/BR(A) has Lys-534 and HPA-5B/BR(B) has Glu-534. HPA-5B is involved in neonatal alloimmune thrombocytopenia (WAIT or NATP). The K534B polymorphism may play a role in coronary artery disease (CAD).
- SIMILARITY: Delongs to the integrin alpha chain family.
- SIMILARITY: Contains 1 WWPA domain.
- SIMILARITY: Contains 1 WWPA domain.
- SIMILARITY: Contains 1 WPA domain.
- SIMILARITY: Contains 1 FG-GAP respects.
- BATABABE: NAME=PROW; NOTE=CD guide CD49b entry;
- WWW="http://www.ncbi.nlm.nlm.gov/prow/cd/cd49b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        COLLAGEN. IT IS RESPONSIBLE FOR ADHESION OF PLATELETS AND OTHER EXELLS TO COLLAGENAS, MODULATION OF COLLAGEN AND COLLAGENASE GENE EXPRESSION, PORCE GENERATION AND ORGANIZATION OF NEWLY SYNTHESIZED EXTRACELLULAR MATRIX.
RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-E-R IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Platelet; Signal; Repeat; Calcium; Magnesium; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIN; 192974; -. R GO Cintegrin complex; TAS. GO; GO:0008305; C:integrin complex; TAS. GO; GO:0008305; C:plasma membrane; TAS. GO; GO:0005806; C:plasma membrane; TAS. GO; GO:0005518; F:colladhesion receptor activity; TAS. GO; GO:0007596; P:blood coagulation; TAS. GO; GO:0007397; P:histogenesis and organogenesis; TAS. R GO; GO:0007397; P:histogenesis and organogenesis; TAS. InterPro; IPR00413; Integrin_alpha.

InterPro; IPR00413; Integrin_alpha.

InterPro; IPR002035; WAF A.

Pfam; PP00357; integrin_A; 1.

Ffam; PP00925; waz; 1.

R Ffam; PP00925; waz; 1.

R FFAM; SW00191; Int_alpha; 5.

R SWART; SW00191; Int_alpha; 1.

R PROSITE; PS00234; WWFA; 1.
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POTENTIAL.
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INTERACTION WITH HPSS.
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FG-GAP 6.
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EMBL; AF52556; AAM34795.1; --
PIR; A33998; A33998.
PDB; 1A0X; 25-NOV-98.
PDB; 1DZI; 02-AUG-01.
Genew; HGNC,6137; ITGA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATES WITH BETA-1.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: Widely expressed with highest expression in muscle and heart. Found in articular cartilage.
-!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colono1305; C:integrin complex; TAS.

RGO; GO:0004895; P:cell adhesion receptor activity; TAS.

RO; GO:0004895; P:cell adhesion receptor activity; TAS.

RGO; GO:000160; P:cell-matrix adhesion; TAS.

RGO; GO:000160; P:cell-matrix adhesion; TAS.

RICEPPO; PR001305; VWF A.

RICEPPO; PR00139; RG-GAP; 3.

REAM; PF01189; RG-GAP; 3.

REAM; PR01189; RG-GAP; 3.

REAM; SMO0191; Int_alpha; 4.

SMART; SM00191; Int_alpha; 4.

SMART; SM00191; Int_alpha; 4.

SMART; SM00191; Int_alpha; 4.

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SMART; SM0191; Int_alpha; 4.

SMART; SM0191; Int_alpha; 4.

SMART; Call adhesion; Receptor; Glycoprotein; Transmembrane;

R SIGNAL; Receptor; Calcium; Magnesium.

SIGNAL; RECEPTOR CALCIUM; Magnesium.

SIGNAL; RECEPTOR CALCIUM; Magnesium.
                                                                                                                                                                                                    "Isolation, cloning, and sequence analysis of the integrin subunit abhiato, a betal-associated collagen binding integrin expressed on chondrocytes.";

J. Biol. Chem. 273:20383-20389 (1998).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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28-F3B-2003 (Rel. 41, Last annotation update)
Integrin alpha-10 precursor.
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TISSUE=Articular chondrocytes;
MEDLINE=98352078; PubMed=9685391;
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EMBL; AF112345; AAF21944.1; --
EMBL; AF172723; AAF61638.1; --
EMBL; AF772723; AAF61638.1; --
GEN, P17301; 1AOX.
Genew; HGNC.6135; ITGA10.
                                                   Homo sapiens (Human)
                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 QIFLERLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRETK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 GSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDS--- 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 FNLDEHHPRLPPGPPEARFGYSVLQHVGGGQRWMLVGAPWDGPSGDRRGDVYRCPVGGAH
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909 G -> V (IN REF. 2).
926 E -> D (IN REF. 2).
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Search completed: June 7, 2004, 17:12:47 Job time: 14.9719 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

Description	Q9ji30 rattus norv O8ca73 mus musculu	Q28984 sus scrofa Osiva6 homo sanien	Ogach4 mus musculu	Q9qye7 rattus norv	Q9wtv4 mus musculu	Q9r200 mus musculu	098tfl cyprinus ca	Q96hbl homo sapien	Q98tf0 cyprinus ca	Q8hzv0 bos taurus	O88340 rattus norv	O88341 rattus norv	Q7tgc3 mus musculu	042094 gallus gall
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% Query Match	74.3	9.49	26.3	55.0	25.9	25.7	23.7	23.0	22.9	21.6	19.6	18.8	17.7	17.7
Score	4371	3799.5	3310,5	3236.5	1523.5	1513	1395	1350.5	1344.5	1269	1154.5	1109	1043.5	1041
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ALIGNMENTS

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D 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

D 01-0M-2003 (TrEMBLrel. 15, Last sequence update)

D 101-0M-2003 (TrEMBLrel. 24, Last annotation update)

D 101-0M-2003 (TrEMBLrel. 24, Last annotation update)

D 101-0M-2003 (TrEMBLrel. 24, Last annotation update)

D 201-0M-2003 (TrEMBLrel. 24, Last annotation update)

D 32 AMBLA POLOGI (REAL)

Nammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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R FRABIL, AZE6893; AAP81280.1; -..

DR SQUENCE FROM N.A.

R FRABIL, AZE6893; AAP81280.1; -..

DR CO; CO:0004895; F:cell adhesion receptor activity; IBA.

DR PEAM; PRO08305; Cintegrin complex; IEA.

DR PEAM; PRO0835; VWFADOMAIN.

DR PEAM; PRO0835; VWFADOMAIN.

DR PEAM; PRO0835; VWFADOMAIN.

DR PRINTS; PRO0455; VWFADOMAIN.

DR PRANT; SMO0191; Int_AIPHA; 1.

DR PRANT; SMO0191; Int_AIPHA; 1.

DR PRANT; SMO0191; Int_AIPHA; 1.

DR PRANT; SMO0191; Int_AIPHA; 1.

SQ SEQUENCE 1151 AA; 126943 MW; 9F785695D4074CAS CRC64;

Query Match

Best Local Similarity 72.64; Pred. No. 1.99-313;

Matches 826; Conservative 150; Mismatches 159; Indels 2; Gaps
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RA THE PARTOM CONSORTIUM,

RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RA THE RIKEN GENOME Exploration of Unctional annotation of RT 60,770 full-length CDNAs.;

REMBL; AR039444; BAC30350.1; -.

REMBL; AR039444; BAC30350.1; -.

REMBL; AR039444; BAC30350.1; -.

REMBL; AR03944; BAC30350.1; -.

REMBL; AR03944; BAC30350.1; -.

REMBL; PROG37; PTOG33.

REMBL; PTOG37; PTOG33.

REMBL; PTOG37; PTOG33.

REPORTOR: PROMO913; Integrin alpha.

REPORTOR: PROMO913; Integrin alpha.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.1%; Score 3891.5; DB 11; Length 1036; Best Local Similarity 66.0%; Pred. No. 4.3e-270; Matches 751; Conservative 125; Mismatches 143; Indels 119;
                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                     RLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                                                                           FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
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GO; GO:0007160; P:cell-adhesion receptor activity; IEA.
InterPro; IPR00413; Integrin_alpha.
InterPro; IPR00183; WWF_A.
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78.8%; Pred. No. 2.2e-271;
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Matches 726; Conservative
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C28984; C1-EMBLrel. 01, Created)
C1-NOV-1996 (TrEMBLrel. 02, Last sequence update)
C1-FEB-1997 (TrEMBLrel. 24, Last sequence update)
C011b (Fragment).
C011b.
Sus scrofa (Fig).
Enkaryota, Metazoa; Chordata, Craniata; Vertebrata; Eut
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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                                                                                                     EBFRIHFTFKBFQNNFNPRSLIKPITQLLGRTHTATGLRKVVRBLFNITNGARKNAFKIL
                                                                         QINNERALKTIQNQLREKI PAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYD
                                                                                                                                                           241 WAGGAFLEMPKDRVIFINTTRVDSDMNDAYLGYAVEVILRNQAQSLVLGAPRYQHTGLVV
                                                                                                                                                                                                                                                                              PQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYS
                                        POKFPEALRGCPOORSDIAFLIDGSGSINRLDFORMKBFVSTVMGOFOKSKTLFALMOYS
                                                                                                                                                                                           WAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVA
                                                                                                                                                                                                                                     MPRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSV
                                                                                                                                                                                                                                                RSQPVLRVKAIMBPNPRBVARNVPECNDQVVKGKEAGBVRVCLHVQKSTRDRLREGQIQS
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                                         378 GAPLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQSLVLGAPRYQHTGKAVIFT
                                                                                                                                                          HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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                                                                                                                                                                                                                                                 PRGQRARWQCDAVLYGBQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 SQGTWSTSCRINHLIFRGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960 VRINGTVINDRPQVTFSBNLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                          421 ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
Tsuchiya H.,
"Isolation of Genes Selectively Expressed by Dendritic Cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF211864; AAF23492.1; -.
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae,
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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Q90XH4;
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TEFOLELPURYANYVVVTSLEVSTRYFNFTASEKTRHVIEHQYQFNNLGQRKLPISVVFW 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFEALKTIONOLREKIFAIEGTOTGSSSSFEHEMSOEGFSAAITSNGPLLSTVGSYDWAG 360
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                                                                                       VPVRLNQTVI WDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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.larity 61.0%; Pred. No. 7.2e-247;
Conservative 142; Mismatches 292; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Integrin, alpha X (Antigen CD11C (p150), alpha polypeptide)
Homo sapiers (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1169 AA; 128521 MW; A17B484FEFC79EB6 CRC64;
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Tiscustering from N.A.

Strausberg R.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ dat

EMBL; BC038237; AAH38237.1; -

GO; GO:0008305; C:integrin complex; IEA.

GO; GO:00074895; P:cell adhesion receptor activity

GO; GO:00074895; P:cell-marxix adhesion; IEA.

InterPro; IPR00413; Integrin_alpha.

InterPro; IPR002035; VWF_A.

Pfam; PF00357; integrin_A; 1.

Pfam; PF00357; integrin_A; 1.

PRINTS; PR01185; INTEGRINA.

SMART; SM00327; VWA; 1.

PROSITE; PS00242; INTEGRINA.

PROSITE; PS00242; INTEGRINA.

PROSITE; PS00242; INTEGRINA.
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                                                                                                                                                                                                                 DIPFFGIORBFNATLKGNLSF 1038
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                    900 DIPSFGIQEELKVTLKGNLSF 920
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Matches 689; Conserv
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Q81VA6

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                                                                                                                                                                                                                                                                                   SIPISLVPILVPVRLNQTVINDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCS 1008
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   796 SDLELNVDVTVSNDGEDSYGTTVTLFYPVGLSFRRVARGQVFLRKCEDQQWQRRGQHSLH
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                                                                                                                                     LACESASSTEVSGALKSTSCSINHPIPPENSEVTPNITFDVDSKASLGNKLLLKANVTSE
                                                                                                                                                                                                            NAMPRINKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTASE-NTSRVMQHQYQVSNLGQR
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.0%; Score 3236.5; DB 11; Length 1161; Best Local Similarity 57.5%; Pred. No. 1.3e-229; Matches 648; Conservative 163; Mismatches 303; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dawley;
A O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.; VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.; VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.; VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.; VanderVieren M., Kilgannon P.D., Dietsch G.,
I Submitted (Aufo-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF021334; AAF21241.1; ---
ROS, GO:00004895; F.Lantegrin Complex; IEA.
R GO: GO:00007160; P:cell adhesion receptor activity; IEA.
R GO: GO:00007160; P:cell adhesion receptor activity; IEA.
R GO: GO:0000725; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR002035; VWF A.
R Pfam; PF004037; integrin_alpha.
R Pfam; PF004037; integrin_alpha.
R Pfam; PF004037; integrin_A; 1.
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                                                           781 GPREFNVTVTVRVRNDGEDSYRTQVTFFFFLDLSYRKVSTLQ-
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PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
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         R MGD; MGI:96609; ILGGAX.

R GO; GO:0003305; C:integrin complex; IEA.

R GO; GO:0004895; F:cell addesion receptor activity; IEA.

R GO; GO:0007229; F:cell-matrix adhesion; IEA.

GO; GO:0007229; P:integrin_mediated signaling pathway; IEA.

R InterPro; IRR000413; Integrin_alpha.

R Pfam; PF00393; FG-GAP; 3.

R Pfam; PF00393; FG-GAP; 3.

R Pfam; PF00302; vwa; 1.

R PRINTS; PR00185; INTEGRINA.

R PRINTS; PR00185; INTEGRINA.

R SMART; SM00191; Int_alpha; 4.

SMART; SM0031; INT; INTEGRINA.

R PROSTTE; PS00242; INTEGRIN_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.3%; Score 3310.5; DB 11; Lengt Best Local Similarity 56.6%; Pred. No. 4.4e-235; Matches 645; Conservative 173; Mismatches 303; Indels
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HSSP; P11215; 1BHQ
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SEQUENCE
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